

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 09:29:50 ; Search time 2881.61 Seconds
(without alignments)
5359.429 Million cell updates/sec

Title: US-10-014-743-3
Perfect score: 738
Sequence: 1 ATACGACTCACTATAGGCG.....CTCACGCTGTAGTATCTCA 738

Scoring table: IDENTITY_NUC
Gap 10.0 , Gapext 1.0
Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_ov.*
- 5: gb_pat.*
- 6: gb_ph.*
- 7: gb_pl.*
- 8: gb_pr.*
- 9: gb_ro.*
- 10: gb_sts.*
- 11: gb_sy.*
- 12: gb_un.*
- 13: gb_vl.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB ID Description

1	738	100.0	738	6	AR036905	AR036905	738 bp	DNA	linear	PAT 29-SEP-1999
2	738	100.0	738	6	AR141144	AR141144				
3	723	98.0	972	12	AX046223	AX046223				
4	723	98.0	2743	12	CVP6M32	CVP6M32				
5	723	98.0	3197	12	CVP6M32FM	CVP6M32FM				
6	723	98.0	3197	12	CVP6M32P	CVP6M32P				
7	705.8	95.6	2746	12	SYNBLUEV	SYNBLUEV				
8	705.8	95.6	3204	12	SYNBLM13M	SYNBLM13M				
9	705.8	95.6	3204	12	SYNBLM13PV	SYNBLM13PV				
10	691.8	93.7	3216	6	AX06816	AX06816				
11	691.8	93.7	3216	6	AX188572	AX188572				
12	689.4	93.4	8126	6	AX085555	AX085555				
13	684.8	92.8	2746	12	CVP6M4Z	CVP6M4Z				
14	682	92.4	3617	12	AF062079	AF062079				
15	679	92.0	3946	12	AF134573	AF134573				
16	678.8	92.0	2890	12	SYNT7T3A19	SYNT7T3A19				
17	677.8	91.8	2862	12	PT219RCS	PT219RCS				
18	677.8	91.8	2862	12	PT219UCS	PT219UCS				
19	677.2	91.8	3394	12	AF062083	AF062083				
20	677.2	91.8	3394	12	AF083409	AF083409				
21	676.8	91.7	4154	12	AF062082	AF062082				
22	676.6	91.7	4503	12	AF062081	AF062081				
23	676.6	91.7	4795	12	AF134572	AF134572				
24	675.6	91.5	3604	12	AF062078	AF062078				
25	675.6	91.5	3604	12	AF083407	AF083407				
26	675.6	91.5	4026	12	AF062080	AF062080				
27	674.6	91.4	3714	12	AF083408	AF083408				
28	674	91.3	3257	12	AF310245	AF310245				
29	672.4	91.1	4283	6	163120	163120				
30	672.4	91.1	4283	6	185496	185496				
31	669	90.7	3179	12	CVGEM132P	CVGEM132P				
32	669	90.7	4118	6	A93963	A93963				
33	669	90.7	4118	6	A93964	A93964				
34	668.2	90.5	2870	12	SYNPT219R	SYNPT219R				
35	668.2	90.5	5621	12	CVU14118	CVU14118				
36	668	90.5	3221	12	CVGEM112M	CVGEM112M				
37	668	90.5	3221	12	CVGEM112P	CVGEM112P				
38	668	90.5	4931	12	CVPGEM1UC	CVPGEM1UC				
39	667.8	90.5	4539	6	AR017907	AR017907				
40	667.8	90.5	4539	6	118794	118794				
41	667.2	90.4	9983	12	HLFINSVECA	HLFINSVECA				
42	667	90.4	2997	12	CVGEM72FP	CVGEM72FP				
43	667	90.4	2998	12	CVGEM72FM	CVGEM72FM				
44	667	90.4	3000	12	CVGEM52FP	CVGEM52FP				
45	667	90.4	3001	12	CVGEM52FM	CVGEM52FM				

ALIGNMENTS

RESULT	1	AR036905	Sequence 3 from patent US 5800996.	738 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR036905	Sequence 3 from patent US 5800996.					
DEFINITION	AR036905	Sequence 3 from patent US 5800996.					
ACCESSION	AR036905	Sequence 3 from patent US 5800996.					
VERSION	AR036905.1	GI:5954761					
KEYWORDS	AR036905.1	GI:5954761					
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 738)						
AUTHORS	Lee,L.G., Spurgeon,S.L. and Rosenblum,B.						
TITLE	Energy transfer dyes with enhanced fluorescence						
JOURNAL	Patent: US 5800996-A 3 01-SEP-1998;						
FEATURES	Location/Qualifiers						
source	1..738						
BASE COUNT	170 a	208 c	192 g	168 t			
ORIGIN	/organism="unknown"						

Query Match 100.0%; Score 738; DB 6; Length 738;
Best Local Similarity 100.0%; Pred. No. 9.7e-198;

	Matches	738;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	ATACGACTCACTATAGGCGGAATTCGAGCTCGGTACCCGGGATCCTCTAGAGTGCACCT	60							
Db	1	ATACGACTCACTATAGGCGGAATTCGAGCTCGGTACCCGGGATCCTCTAGAGTGCACCT	60							
QY	61	GCAGGCATGCAAGCTTGAGTATTCATAGTGTACCTAATAGCTTGGCGTAACTCATGGT	120							
Db	61	GCAGGCATGCAAGCTTGAGTATTCATAGTGTACCTAATAGCTTGGCGTAACTCATGGT	120							
QY	121	CATAGCTGTTTCCTGTGTGAATTTGTTATCCGCTCACAATTCACACAACA..CGAGCGC	180							
Db	121	CATAGCTGTTTCCTGTGTGAATTTGTTATCCGCTCACAATTCACACAACAATAGAGCGC	180							
QY	181	GAAGCATAAAGTCTAAAGCTTGGGTGGCTTAATGAGTGAGCTAACTCACATTAATTCGGT	240							
Db	181	GAAGCATAAAGTCTAAAGCTTGGGTGGCTTAATGAGTGAGCTAACTCACATTAATTCGGT	240							
QY	241	TGGCCTACTGCCGCTTTCCAGTCGGGAACCTGTCGTGCAGCTGCATTAATGAATCG	300							
Db	241	TGGCCTACTGCCGCTTTCCAGTCGGGAACCTGTCGTGCAGCTGCATTAATGAATCG	300							
QY	301	GCCACGCGCGGGAGAGCGGTTTGGCGTATGGGCGCTCTTCGGCTTCCTCGCTCACTG	360							
Db	301	GCCACGCGCGGGAGAGCGGTTTGGCGTATGGGCGCTCTTCGGCTTCCTCGCTCACTG	360							
QY	361	ACTCGTGGCGTTCGTCGTTGGCTTGGCGGAGCGGTATCAGCTCACTCAAGGCGGTAA	420							
Db	361	ACTCGTGGCGTTCGTCGTTGGCTTGGCGGAGCGGTATCAGCTCACTCAAGGCGGTAA	420							
QY	421	TACGGTTATCCACAGAAATCAGGGATACGCGAGAAAGACATGTGAGCAAAAGGCCAGC	480							
Db	421	TACGGTTATCCACAGAAATCAGGGATACGCGAGAAAGACATGTGAGCAAAAGGCCAGC	480							
QY	481	AAAGGCCAGAAACCGTAAAGAGCCCGCTTGCTGGCGTTTTCATAGCTTCGCGCCCGC	540							
Db	481	AAAGGCCAGAAACCGTAAAGAGCCCGCTTGCTGGCGTTTTCATAGCTTCGCGCCCGC	540							
QY	541	CTGACGAGCATCACAANAATCGAGCGTCAAGTCAGAGGTGGCGAAACCCGACAGACTAT	600							
Db	541	CTGACGAGCATCACAANAATCGAGCGTCAAGTCAGAGGTGGCGAAACCCGACAGACTAT	600							
QY	601	AAAGATACGAGGCGTTTCCCGCTTGAAGCTCCCTCGTGGCTTCCTCTCGGACCCCTGC	660							
Db	601	AAAGATACGAGGCGTTTCCCGCTTGAAGCTCCCTCGTGGCTTCCTCTCGGACCCCTGC	660							
QY	661	CGCTTACCGGATACCTGTCGGCTTCTCCCTTCCGGAAGCGTGCGCTTTCTCATAGCT	720							
Db	661	CGCTTACCGGATACCTGTCGGCTTCTCCCTTCCGGAAGCGTGCGCTTTCTCATAGCT	720							
QY	721	CACGCTGTAGGTATCTCA	738							
Db	721	CACGCTGTAGGTATCTCA	738							

RESULT	2
ARI411144	
LOCUS	
DEFINITION	ARI411144
ACCESSION	Sequence 3 from patent US 6145434.
VERSION	ARI411144
KEYWORDS	ARI411144.1 GI:15100661
	738 bp DNA
	linear PAT 08-AUG-2001

ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 738)
TITLE	Tanaka, T. and Kobayashi, K.
JOURNAL	Stencil printing method and device
FEATURES	Patent: US 6145434-A 3 14-Nov-2000;
SOURCE	Location/Qualifiers 1 738

BASE COUNT	/organism="unknown"
170 a	208 c
	192 g
	168 t

1. The first step in the process is to identify the problem or issue that needs to be addressed. This involves gathering information and understanding the context of the problem.

ORIGIN

Query Match	100.0%;	Score 738;	DB 6;	Length 738;
Best Local Similarity	100.0%;	Pred. No. 9,7e-198;		
Matches 738; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	ATACGACTCACTATAGGGCGAATTCGAGCTCGGTACCCGGGATCCTCTAGAGTCGACCT	60		
DB 1	ATACGACTCACTATAGGGCGAATTCGAGCTCGGTACCCGGGATCCTCTAGAGTCGACCT	60		
QY 61	GCAGGCATCAAGCTTGAGTATTCTATAGTGTCACTTAATAGCTTGGCGTAATCATGGT	120		
DB 61	GCAGGCATCAAGCTTGAGTATTCTATAGTGTCACTTAATAGCTTGGCGTAATCATGGT	120		
QY 121	CATAGCTGTTTCCCTGTGTGAATTTGTTATCCGCTCACAATTCACACAAACATAGAGCG	180		
DB 121	CATAGCTGTTTCCCTGTGTGAATTTGTTATCCGCTCACAATTCACACAAACATAGAGCG	180		
QY 181	GAAGCATCAAGTGTAAAGCCCTGGGGTGCGCTAATGAGTGAGCTAACTCAATTAATTCGCT	240		
DB 181	GAAGCATCAAGTGTAAAGCCCTGGGGTGCGCTAATGAGTGAGCTAACTCAATTAATTCGCT	240		
QY 241	TGCGCTCACTCCCGCTTTCCAGTCGGGAAACCTTGTCTGCACGCTGCATTAATGAATCG	300		
DB 241	TGCGCTCACTCCCGCTTTCCAGTCGGGAAACCTTGTCTGCACGCTGCATTAATGAATCG	300		
QY 301	GCCAAAGCGGGGAGAGGCGGTTTGCGTATTTGGGCGCTCTTCGCGTTCCTCGCTCACTG	360		
DB 301	GCCAAAGCGGGGAGAGGCGGTTTGCGTATTTGGGCGCTCTTCGCGTTCCTCGCTCACTG	360		
QY 361	ACTCGCTGCGTCGGTTCGTTCCGCTCGCGCGAGCGGTTTGCGTATTTGGGCGCTCTTCGCGTTCCTCGCTCACTG	420		
DB 361	ACTCGCTGCGTCGGTTCGTTCCGCTCGCGCGAGCGGTTTGCGTATTTGGGCGCTCTTCGCGTTCCTCGCTCACTG	420		
QY 421	TACGGTTATCCACAGAAATCAGGGGATAACCCAGGAAGAACATGTGAGCAAAAGGCCAGC	480		
DB 421	TACGGTTATCCACAGAAATCAGGGGATAACCCAGGAAGAACATGTGAGCAAAAGGCCAGC	480		
QY 481	AAAAGCCAGGAACCGTAAAAAGGCGCGTTGCTGGCGTTTTCATAGGCTCCGCGCCC	540		
DB 481	AAAAGCCAGGAACCGTAAAAAGGCGCGTTGCTGGCGTTTTCATAGGCTCCGCGCCC	540		
QY 541	CTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGTGGCGAAACCCGACGACTAT	600		
DB 541	CTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGTGGCGAAACCCGACGACTAT	600		
QY 601	AAAGATACAGCGGTTTCCCTGGAAGTCCTCGTCGCTCTCCTCTGTCGACCCCTGC	660		
DB 601	AAAGATACAGCGGTTTCCCTGGAAGTCCTCGTCGCTCTCCTCTGTCGACCCCTGC	660		
QY 661	CGCTTACCGGATACCTGTCGCGCTTTCCTTCGGGAAGCGTGGCGTTTCTCATAGCT	720		
DB 661	CGCTTACCGGATACCTGTCGCGCTTTCCTTCGGGAAGCGTGGCGTTTCTCATAGCT	720		
QY 721	CACGCTGTAGGTATCTCA 738			
DB 721	CACGCTGTAGGTATCTCA 738			

RESULT	3
AX046223	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	

Diagnostic sequencing by a combination of specific cleavage and

mass spectrometry
Patent: WO 0066771-A 3 09-NOV-2000;
Methexis N.V. (BE)
Location/Qualifiers
1..972
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic-pGEM3-2f(+) derived nucleotide"
BASE COUNT 217 a 272 c 261 g 222 t
ORIGIN

Query Match 98.0%; Score 723; DB 6; Length 972;
Best Local Similarity 100.0%; Pred. No. 1.7e-193; Gaps 0;
Matches 723; Conservative 0; Mismatches 0; Indels 0;

Qy 16 GGGCGAATTCGAGTCGATCCCGGGATCCTCTAGAGTCGACCTGCGAGCATGCAAGCT 75
Db 1 GGGCGAATTCGAGTCGATCCCGGGATCCTCTAGAGTCGACCTGCGAGCATGCAAGCT 60

Qy 76 TGAGTATTCATAGTGTACCTAAATAGCTTGGCGTAATCATGTCATAGCTCTTTCCCTG 135
Db 61 TGAGTATTCATAGTGTACCTAAATAGCTTGGCGTAATCATGTCATAGCTCTTTCCCTG 120

Qy 136 TGTGAATTTGTTATCGCTCACAATTCACACACATACGAGCGCGAAGCATAAAGTGA 195
Db 121 TGTGAATTTGTTATCGCTCACAATTCACACACATACGAGCGCGAAGCATAAAGTGA 180

Qy 196 AAGCTTCGGGTGCTTAATGAGTGAGTAACTCACAATTAATTCGCTTCGCTCACTGCGCG 255
Db 181 AAGCTTCGGGTGCTTAATGAGTGAGTAACTCACAATTAATTCGCTTCGCTCACTGCGCG 240

Qy 256 CTTTCCAGTCGGGAACCTGTGTCGACGCTGCAATTAATGAATGCGGCACAGCGCGCGGA 315
Db 241 CTTTCCAGTCGGGAACCTGTGTCGACGCTGCAATTAATGAATGCGGCACAGCGCGCGGA 300

Qy 316 GAGCGGTTTTCGATTTGGCGCTCTTCGCGTTCCTCGCTCACTGCTGCGCTGCGTCGG 375
Db 301 GAGCGGTTTTCGATTTGGCGCTCTTCGCGTTCCTCGCTCACTGCTGCGCTGCGTCGG 360

Qy 376 TCGTTTCGCTGCGCGAGCGGTATACGCTCACTCAAGCGGTAAATACGGTTATCCACAG 435
Db 361 TCGTTTCGCTGCGCGAGCGGTATACGCTCACTCAAGCGGTAAATACGGTTATCCACAG 420

Qy 436 AATCAGGGGATACGCGAGGAAGCAATGTGAGCAAAAGCGGACGAAAGGCCAGGAACC 495
Db 421 AATCAGGGGATACGCGAGGAAGCAATGTGAGCAAAAGCGGACGAAAGGCCAGGAACC 480

Qy 496 GTAAAGCGCGCTGCTGCGCTTTTTCATAGGCTCGCCCGCTGACGAGCATCACA 555
Db 481 GTAAAGCGCGCTGCTGCGCTTTTTCATAGGCTCGCCCGCTGACGAGCATCACA 540

Qy 556 AAAATCGAGCTCAAGTCAGAGTGGCGAAACCCGACAGGATATAAGATACAGCGGT 615
Db 541 AAAATCGAGCTCAAGTCAGAGTGGCGAAACCCGACAGGATATAAGATACAGCGGT 600

Qy 616 TTCCCGCTGGAAGTCCCTGCTGCGCTCTCTGTTCCGACCTCGCGCTTACCGGATACC 675
Db 601 TTCCCGCTGGAAGTCCCTGCTGCGCTCTCTGTTCCGACCTCGCGCTTACCGGATACC 660

Qy 676 TGTCCGCTTTCTCCCTTCGGAAGCGGTGCGCTTCTCATAGCTCACTGCTAGGTATC 735
Db 661 TGTCCGCTTTCTCCCTTCGGAAGCGGTGCGCTTCTCATAGCTCACTGCTAGGTATC 720

Qy 736 TCA 738
Db 721 TCA 723

RESULT 4
CVPGEM32
LOCUS
DEFINITION Cloning vector pGEM-32. 2743 bp DNA circular SYN 18-FEB-2000

ACCESSION X65304.3 GI:7018282
VERSION beta-lactamase; bla gene; cloning vector; lacZ gene; multiple
KEYWORDS cloning site; promoter.
SOURCE Cloning vector pGEM-32.
ORGANISM Cloning vector pGEM-32.
REFERENCE 1 (bases 1 to 2743)
AUTHORS Technical Services,
TITLE Direct Submission
JOURNAL 2800 Woods Hollow Road, Madison, WI 53711-5399, USA
REMARK revised by [2]
AUTHORS Technical Services,
TITLE Direct Submission
JOURNAL 2800 Woods Hollow Road, Madison, WI 53711-5399, USA
REMARK revised by [3]
AUTHORS Technical Services,
TITLE Direct Submission
JOURNAL 2800 Woods Hollow Road, Madison, WI 53711-5399, USA
REMARK revised by [4]
AUTHORS Technical Services,
TITLE Direct Submission
JOURNAL 2800 Woods Hollow Road, Madison, WI 53711-5399, USA
COMMENT This vector can be obtained from Promega Corporation, Madison, WI.
Call one of the following numbers for order or technical information:
Order or Technical 800-356-9526
In Wisconsin 800-356-9526
Outside U.S. 608-274-4330.

FEATURES
source 1..2743
/organism="Cloning vector pGEM-32"
/db_xref="taxon:90110"
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/note="T7 transcription initiation site"
misc_feature 5..61
/note="multiple cloning sites"
promoter 67..86
/note="SP6 promoter"
misc_feature 69
/note="SP6 transcription initiation site"
primer_bind complement(104..120)
/note="pUC/M13 reverse sequencing primer"
misc_feature complement(106..108)
/gene="lacZ"
gene /note="lacZ start codon"
complement(106..108)
/gene="lacZ"
misc_feature 128..144
/note="lac operator"
gene complement(1265..2125)
/gene="bla"
CDS complement(1265..2125)
/gene="bla"
/codon_start=1
/transl_table=11
/product="beta-lactamase"
/protein_id="CAA46396.2"
/db_xref="GI:6782313"
/translation="MSIQHFRVALIPFFAFLPFAHPETLVKVKDAEDQLGARVGY
IELDLNSGKILSFEPFRFPMNSFVLLCAGVLSIRADGQEQGLGRIRHYSDVNLVE
YSPVTEKHLTDGNTVPKELCSAAITMSDNTAANLLLTITGGPKELTFLHNMADKVGPL
DRPEELNEAI PNDERTTTPVMAATTTLKLLTGLTLLASRQQLIDMEADKVGPL
LRSALPAGFIADKSGAGERSGIIAALGPDGKPSRIIVYITTSQATMDERNROIA

misc_feature
primer_bind
promoter
BASE COUNT 685 a 685 c 696 g '77 t
ORIGIN

EIGASLIKHW

join(2561..2724,94..323)
/note="lac operon sequence"
2684..2700
/note="pUC/M13 forward sequencing primer"
join(2727..2743,1..3)
/note="T7 promoter"

Query Match 98.0% Score 7 DB 12: 743;
Best Local Similarity 100.0% Pred 1.7e-1
Matches 723; Conservative 0; Mismatches 0; Indelets 0; Gaps 0;

QY 16 GGGCGAATTCGAGCTCGGTACCGGGATCCTTAGAGTCGACCTGACGGCATGCAAGCT 75
Db 1 GGGCGAATTCGAGCTCGGTACCGGGATCCTTAGAGTCGACCTGACGGCATGCAAGCT 75
QY 76 TGAGTATTCATAGTGCACCTAAATAGCTTGGCGTAATCATGTCATAGCTGTTCTCGT 135
Db 61 TGAGTATTCATAGTGCACCTAAATAGCTTGGCGTAATCATGTCATAGCTGTTCTCGT 135
QY 136 TGTGAATTTGTTATCGCTCAACATTCACACACATACGAGCGGGAAGCATAAAGTGA 195
Db 121 TGTGAATTTGTTATCGCTCAACATTCACACACATACGAGCGGGAAGCATAAAGTGA 195
QY 196 AAGCGTGGGTGCTTAATGATGAGCTAACTCACTAAATTTGGCTTGCCTCACTGCCG 255
Db 181 AAGCGTGGGTGCTTAATGATGAGCTAACTCACTAAATTTGGCTTGCCTCACTGCCG 255
QY 256 CTTTCCAGTCGGGAACCTGTCGTCGAGCTGCAATTAATTCGGCCCAACGCGGGGA 315
Db 241 CTTTCCAGTCGGGAACCTGTCGTCGAGCTGCAATTAATTCGGCCCAACGCGGGGA 315
QY 316 GAGGGGTTTGGCTATTTGGGCTTTCCTGCTTCTGCTCACTGCTGCTGCTGCTG 375
Db 301 GAGGGGTTTGGCTATTTGGGCTTTCCTGCTTCTGCTCACTGCTGCTGCTGCTG 375
QY 376 TCGTTCGCTCGCGGAGCGGTATCAGCTCACTCAAGCGGTAAATACGGTTATCCAC 435
Db 361 TCGTTCGCTCGCGGAGCGGTATCAGCTCACTCAAGCGGTAAATACGGTTATCCAC 435
QY 436 AATCAGGGGTAACGCGAGGAACCAATCTGAGCAAAAGCGGCAAGCCAGGCAAC 495
Db 421 AATCAGGGGTAACGCGAGGAACCAATCTGAGCAAAAGCGGCAAGCCAGGCAAC 495
QY 496 GTAAAGGCGGCTTCTGCTGCTGCTTTCATAGGCTCGGCGCTTTCATAGGCTCG 555
Db 481 GTAAAGGCGGCTTCTGCTGCTGCTTTCATAGGCTCGGCGCTTTCATAGGCTCG 555
QY 556 AAATCAGCGCTCAAGTCAGAGTGGCGAAGCCGACAGGACTATAAGATACGAGCGT 615
Db 541 AAATCAGCGCTCAAGTCAGAGTGGCGAAGCCGACAGGACTATAAGATACGAGCGT 615
QY 616 TTCCCGCTGGAAGCTCCCTGCTGCTGCTTTCATAGGCTCGGCGCTTTCATAGGCT 600
Db 601 TTCCCGCTGGAAGCTCCCTGCTGCTGCTTTCATAGGCTCGGCGCTTTCATAGGCT 600
QY 676 TGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCATAGCTACGCTGAGGTATC 735
Db 661 TGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCATAGCTACGCTGAGGTATC 735
QY 736 TCA 738
Db 721 TCA 723

RESULT 5
CVGEM32FM
LOCUS
DEFINITION Cloning vector pGEM-3zf(-).
ACCESSION X65307

VERSION
KEYWORDS
SOURCE
ORGANISMREFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNALREMARK
AUTHORS
TITLE
JOURNALREMARK
AUTHORS
TITLE
JOURNAL

COMMENT

X65307.2 GI:8216946
beta-lactamase; bla gene; cloning vector; lac2 gene; multiple
cloning site; phage f1 region; promoter.
Cloning vector pGEM-3zf(-).
Cloning vector pGEM-3zf(-).
artificial sequence; vectors.
1 (bases 1 to 3197)
Solomon, L.R., Massam, L.R. and Jarrett, H.W.
Enzymatic syntheses of DNA-silicas using DNA polymerase
Anal. Biochem. 203 (1), 58-69 (1992)
92398067
2 (bases 1 to 3197)
Technical Services.
Direct Submission
Submitted (23-MAR-1992) Technical Services, Promega Corporation,
2800 Woods Hollow Road, Madison, WI 53711-5399, USA
revised by [3]
3 (bases 1 to 3197)
Technical Services.
Direct Submission
Submitted (28-MAY-1993) Technical Services, Promega Corporation,
2800 Woods Hollow Road, Madison, WI 53711-5399, USA
revised by [4]
4 (bases 1 to 3197)
Technical Services.
Direct Submission
Submitted (22-MAY-2000) Technical Services, Promega Corporation,
2800 Woods Hollow Road, Madison, WI 53711-5399, USA
On Jun 3, 2000 this sequence version replaced gi:58172.
See X65300-X65335 for related vector sequences
This vector can be obtained from Promega Corporation, Madison, WI.
Call one of the following numbers for order or technical
information:
Order or Technical 800-356-9526
In Wisconsin 800-356-9526
Outside U.S. 608-274-4330.

FEATURES
source

1..3197
/organism="Cloning vector pGEM-3zf(-)"
/db_xref="taxon:90113"

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1
/note="T7 transcription initiation site"

misc_feature
5..61
/note="multiple cloning sites"

promoter
67..86
/note="SP6 promoter"

misc_feature
69
/note="SP6 transcription initiation site"

misc_feature
94..323
/note="lac operon sequence"

primer_bind
complement(104..120)
/note="pUC/M13 reverse sequencing primer"

gene
complement(106..108)
/gene="lacZ"

misc_feature
complement(106..108)
/gene="lacZ"

gene
complement(1265..2125)
/gene="bla"

CDS
complement(1265..2125)
/gene="bla"

transl_table=1
/transl_table=11

product="Beta-lactamase"

protein_id="CAA46399.2"

db_xref="GI:8216947"

translation="MSIQHFRVALIPFFAAFLPFAHPETLVKVKDAEDQLGARVGY
LELDLNSKILESFRPEEPMFTFVLLCGAVLSRIDAGQQLGRRITYSDNDLVE
KSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTIGPKELTFLHMGDHTVRL
RWPEPELNEATIPNDERDTPVAMATTIRKLTLGLTLLASRQQLIDHWDKVAAGPL
LRSLALPAGWFTADKSGAGSGRGIITAAALGPDGPKPSRIIVITIGSQATIDERNRQIA
EIGASLIKHW"

misc_feature
2562..3017

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misc_feature /note="phage fl region"
primer_bind /note="lac operon sequence"
promoter /note="pUC/M13 forward sequencing primer"
join(3181..3197,1..3)
/note="T7 promoter"
BASE COUNT 781 a 806 c 796 g 814 t
ORIGIN
Query Match 98.0%; Score 723; DB 12; Length 3197;
Best Local Similarity 100.0%; Pred. No. 1.7e-193;
Matches 723; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 GGGCAATTCAGCTCGGTACCCGGGATCCTCTAGAGTCGACCTCCAGGCATGCAAGCT 75
Db 1 GGGCAATTCAGCTCGGTACCCGGGATCCTCTAGAGTCGACCTCCAGGCATGCAAGCT 60
QY 76 TGAGTATTCTATAGTGTACCTAATAGCTTGGCTGAATCATGCTATAGCTTTCCCTG 135
Db 61 TGAGTATTCTATAGTGTACCTAATAGCTTGGCTGAATCATGCTATAGCTTTCCCTG 120
QY 136 TGTGAATTTATTCGCTACATTCACACACATACGAGCGGGAAGCATAAAGTGA 195
Db 121 TGTGAATTTATTCGCTACATTCACACACATACGAGCGGGAAGCATAAAGTGA 180
QY 196 AAGCTGGGGTCCCTAATAGTGTACCTAATAGCTTGAATTCGCTTCCCTGCTCCCG 255
Db 181 AAGCTGGGGTCCCTAATAGTGTACCTAATAGCTTGAATTCGCTTCCCTGCTCCCG 240
QY 256 CTTTCAGTTCGGGAACCTGCTGCGAGCTGCATTAATCAATCGGCCACGCGGGGA 315
Db 241 CTTTCAGTTCGGGAACCTGCTGCGAGCTGCATTAATCAATCGGCCACGCGGGGA 300
QY 316 GAGCGGGTTGCGTATTGGGCGCTCTCCGCTTCTCCTGCTACTGCTCGCTCGCTCGG 375
Db 301 GAGCGGGTTGCGTATTGGGCGCTCTCCGCTTCTCCTGCTACTGCTCGCTCGCTCGG 360
QY 376 TCGTTTCGCTGCGGAGCGGTATCAGCTCACTCAAGGCGGTAATACGTTATCCACAG 435
Db 361 TCGTTTCGCTGCGGAGCGGTATCAGCTCACTCAAGGCGGTAATACGTTATCCACAG 420
QY 436 AATCAGGGGATTAACGAGGAAGAACATGTGAGCAAAAGGCCAGCAAGGCCAGGAACC 495
Db 421 AATCAGGGGATTAACGAGGAAGAACATGTGAGCAAAAGGCCAGCAAGGCCAGGAACC 480
QY 496 GTAAAGAGCCGCTGCTGCGGCTTTTTCATAGCTCCGCCGCCCTGACGAGCATCACA 555
Db 481 GTAAAGAGCCGCTGCTGCGGCTTTTTCATAGCTCCGCCGCCCTGACGAGCATCACA 540
QY 556 AAAATCGAGCTCAAGTCAGAGGTGGCGAAACCGCAGAGCACTATAAGATACCAAGCGT 615
Db 541 AAAATCGAGCTCAAGTCAGAGGTGGCGAAACCGCAGAGCACTATAAGATACCAAGCGT 600
QY 616 TTCCCTCCGGAAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 675
Db 601 TTCCCTCCGGAAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 676 TGTCCGCCCTTTCCTCCGGAAGCGTGGCGCTTCTCATAGCTACGCTGAGGTATC 735
Db 661 TGTCCGCCCTTTCCTCCGGAAGCGTGGCGCTTCTCATAGCTACGCTGAGGTATC 720
QY 736 TCA 738
Db 721 TCA 723
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RESULT 6
CVP6EM32P CVP6EM32P 3197 bp DNA circular SYN 16-JUL-1999
LOCUS Cloning vector pGEM-3zf(+).
DEFINITION X65306
ACCESSION
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VERSION X65306.2 GI:5531232
KEYWORDS cloning vector; multiple cloning site; phage fl region; promoter.
SOURCE Cloning vector pGEM-3zf(+).
ORGANISM Cloning vector pGEM-3zf(+)
artificial sequence; vectors.
REFERENCE 1 (bases 1 to 3197)
AUTHORS Solomon, L.R., Massom, L.R. and Jarrett, H.W.
TITLE Enzymatic syntheses of DNA-silicas using DNA polymerase
JOURNAL Anal. Biochem. 203 (1), 58-69 (1992)
MEDLINE 92398067
REFERENCE 2 (bases 1 to 3197)
AUTHORS Technical Services.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-1992) Technical Services, Promega Corporation,
2800 Woods Hollow Road, Madison, WI 53711-5399, USA
REMARK revised by [3]
REFERENCE 3 (bases 1 to 3197)
AUTHORS Technical Services.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-1993) Technical Services, Promega Corporation,
2800 Woods Hollow Road, Madison, WI 53711-5399, USA
REMARK revised by [4]
REFERENCE 4 (bases 1 to 3197)
AUTHORS Kenefick, K.
TITLE Direct Submission
JOURNAL Submitted (14-JUL-1999) Kenefick, K., Technical Services, Promega
Corporation, 2800 Woods Hollow Road, Madison, WI 53711-5399, USA
COMMENT On Jul 19, 1999 this sequence version replaced g1:58203.
See X65300-X65335 for related vector sequences
This vector can be obtained from Promega Corporation, Madison, WI.
Call one of the following numbers for order or technical
information:
Order or Technical 800-356-9526
In Wisconsin 800-356-9526
Outside U.S. 608-274-4330.
FEATURES
source location/Qualifiers
1..3197
/organism="Cloning vector pGEM-3zf(+)"
/db_xref="taxon:90112"
misc_feature 1
/note="T7 transcription initiation site"
misc_feature 5..61
/note="multiple cloning sites"
promoter 67..86
/note="SP6 promoter"
misc_feature 69
/note="SP6 transcription initiation site"
misc_feature 94..323
/note="lac operon sequence"
misc_feature complement(106..108)
/note="lacZ"
gene complement(106..108)
/note="lacZ start codon"
gene complement(1265..2125)
/note="lacZ"
CDS complement(1265..2125)
/note="bla"
/codon_start=1
/transl_table=11
/product="beta-lactamase"
; /protein_id="CAA46398.2"
; /db_xref="GI:5531233"
misc_feature 2582..3017
/note="phage fl region"
misc_feature 3018..3178
/note="lac operon sequence"
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promoter      join(3181..3197,3)
              /note="T7 promoter"
BASE COUNT    822 a 785 c 817 g 773 t
ORIGIN

Query Match      98.0%; Score 723; DB 12; Length 3197;
Best Local Similarity 100.0%; Pred. No. 1.7e-193;
Matches 723; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GGGCGAATTCAGCTCGGTACCGGGGATCTCTAGAGTCGACCTCCAGGCATCAAGCT 75
      |||
Db 1 GGGCGAATTCAGCTCGGTACCGGGGATCTCTAGAGTCGACCTCCAGGCATCAAGCT 60

QY 76 TGAGTATTCATAGTGTACCTAAATAGCTTGGCGTAAATCATGGTCATAGCTGTTTCCTG 135
      |||
Db 61 TGAGTATTCATAGTGTACCTAAATAGCTTGGCGTAAATCATGGTCATAGCTGTTTCCTG 120

QY 136 TGTGAAATTTGTATCCGCTCACAAATCCACAAACATACGAGCGGAAGCATAAAGTGA 195
      |||
Db 121 TGTGAAATTTGTATCCGCTCACAAATCCACAAACATACGAGCGGAAGCATAAAGTGA 180

QY 196 AAGCTGGGTGCTTAATAGTGTAGTCACTACATTAATTCGTTGGCTCACTGCGCG 255
      |||
Db 181 AAGCTGGGTGCTTAATAGTGTAGTCACTACATTAATTCGTTGGCTCACTGCGCG 240

QY 256 CTTTCCAGTCGGGAAAGCTGCTGTCAGCTGCATTAAATGAATCGGCAAGCGCGGGA 315
      |||
Db 241 CTTTCCAGTCGGGAAAGCTGCTGTCAGCTGCATTAAATGAATCGGCAAGCGCGGGA 300

QY 316 GAGCGGTTTGGCTATTGGCGCTCTTCGCTTCTCGCTCACTCACTCGCTGCGCTCGG 375
      |||
Db 301 GAGCGGTTTGGCTATTGGCGCTCTTCGCTTCTCGCTCACTCACTCGCTGCGCTCGG 360

QY 376 TCGTTCGGCTCGCGGAGCGGTATCAGCTCACTCAAAAGCGGTAATACGTTATCCACAG 435
      |||
Db 361 TCGTTCGGCTCGCGGAGCGGTATCAGCTCACTCAAAAGCGGTAATACGTTATCCACAG 420

QY 436 AATCAGGGGATAACGAGGAAAGACATGTAGCAAGAGCCAGCAAGGCGCAGGAACC 495
      |||
Db 421 AATCAGGGGATAACGAGGAAAGACATGTAGCAAGAGCCAGCAAGGCGCAGGAACC 480

QY 496 GTAAAAAGCGGCTTGTGGGCTTTTCCATAGGCTCCGCCGCCCTGACGAGCATCACA 555
      |||
Db 481 GTAAAAAGCGGCTTGTGGGCTTTTCCATAGGCTCCGCCGCCCTGACGAGCATCACA 540

QY 556 AAAATCAGCGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACCAGCGT 615
      |||
Db 541 AAAATCAGCGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACCAGCGT 600

QY 616 TTCCCGCTGGAAGCTCCCTCGTGGCGTCTCTGTTCCGACCCCTGCGGCTTACCGGATACC 675
      |||
Db 601 TTCCCGCTGGAAGCTCCCTCGTGGCGTCTCTGTTCCGACCCCTGCGGCTTACCGGATACC 660

QY 676 TGTCCGCTTTCCTCCCTTCGGAAGCGTGGCGCTTTCATAGCTCAAGCTGTAGGTATC 735
      |||
Db 661 TGTCCGCTTTCCTCCCTTCGGAAGCGTGGCGCTTTCATAGCTCAAGCTGTAGGTATC 720

QY 736 TCA 738
      |||
Db 721 TCA 723

RESULT 7
SYNBLUEV
LOCUS      SYNBLUEV          2746 bp      DNA      circular SYN 16-MAR-2000
DEFINITION BlueScribe cloning vector.
ACCESSION M77811 M77798
VERSION    M77811.1 GI:208035
KEYWORDS   Cloning vector BlueScribe.
SOURCE     Cloning vector BlueScribe.
            artificial sequence; vectors.
ORGANISM   Cloning vector BlueScribe
            /db_xref="taxon:118306"
```

1 (sites)
Short, J.M., Fernandez, J.M., Sorge, J.A. and Huse, W.D.
Lambda ZAP: A bacteriophage lambda expression vector with in vivo
excision properties
Nucleic Acids Res. 16, 7583-7600 (1988)
88319944
2 (bases 1 to 2746)
Gilbert, W.
Obtained from VecBase 3.0
Unpublished
These data and their annotation were supplied to GenBank by Will
Gilbert under the auspices of the GenBank Curator Program.
BlueScribe - Cloning vector
ENTRY BLUE
- Cloning vector
DATE 03-MAR-1986
#sequence 16-DEC-1986
#sequence 02-FEB-1987
ACCESSION VB0042
SOURCE artificial
REFERENCE
#number 1
#authors Fernandez J.M., Short J.M., Renshaw M., Huse W., Sorge
J.
#Journal Gene (1987) in press
#citation sequence data from StrataGene
#comment sequence correction according to StrataGene COMMENT
Obtained 28-JAN-1987 from StrataGene on floppy disc.
Revised 2-FEB-1986 by F. Pfeiffer:
1122/3 'AP' to 'TA' to match revised sequence of pBR322
Revised 4-MAR-1987 to match sequence of pUC19 on request
of StrataGene
COMMENT
The stand shown corresponds to pUC19c.
As in the published sequence of pUC19c, The M13mp19 lac2 region
is on the complementary strand.
KEYWORDS
CROSSREFERENCE
#parent
VecBase(3):pUC19, VecSource(3):PromT7, VecSource(3):PromT3
#offspring
VecBase(3):BlueM13p, VecBase(3):BlueM13m
PARENT
Features of BlueScribe (2746 bp)
residue source
1- 400 684- 281 (c) pUC19
402- 421 1- 20 T7 promoter
423- 479 1- 57 M13mp19/pUC19-polylinker
485- 506 20- 1 (c) T3 promoter
508- 744 237- 1 (c) pUC19
745- 2746 2686- 685 (c) pUC19
Conflict (cfl) and Mutations (mut): none
PARENT
Features of BlueScribe (2746 bp)
residue source
1- 400 1- 400 pUC19c
402- 421 1- 20 T7 promoter
423- 479 57- 1 (c) M13mp19/pUC19-polylinker
485- 506 20- 1 (c) T3 promoter
513- 2746 453- 2686 pUC19c
Conflict (cfl) and Mutations (mut): none
FEATURE
1689-2477 789-1 (c) Ap-R; b-lactamase
POLYLINKER HindIII-SphI-PstI-SalI-XbaI-BamHI-SmaI-KpnI-SacI-EcoRI
SELECTION
#resistance Ap
#indicator beta-galactosidase
SUMMARY Blue #length 2746 #checksum 2145.
Location/Qualifiers
1..2746
/organism="Cloning vector BlueScribe"
/db_xref="taxon:118306"

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/focus
1. 400
/organism="Cloning vector pUC19"
/db_xref="taxon:31851"
402..421
/organism="Enterobacteria phage T7"
/organism="Bacteriophage T7 promoter"
/db_xref="taxon:10760"
423..479
/organism="Cloning vector pUC19"
/db_xref="taxon:31851"
485..506
/organism="Bacteriophage T3"
/organism="Bacteriophage T3 promoter"
/db_xref="taxon:10759"
508..744
/organism="Cloning vector pUC19"
/db_xref="taxon:31851"
745..746
/organism="Cloning vector pUC19"
/db_xref="taxon:31851"
680 a 686 c 700 g 680 t

BASE COUNT
ORIGIN

Query Match 95.6%; Score 705.8; DB 12; Length 2746;
Best Local Similarity 98.0%; Pred. No. 1.2e-188;
Matches 726; Conservative 0; Mismatches 12; Indels 3; Gaps 1;

QY 1 ATACGACTACATAGGCGGAATTCGAGCTCGGTACCGGGAGTCTCTAGAGTCGACCT 60
Db 404 ATACGACTACATAGGCGGAATTCGAGCTCGGTACCGGGAGTCTCTAGAGTCGACCT 463
QY 61 GCAGGCGATCAAGCTTGGATTTCTATAGTGTACCTAAAT---AGCTGGCGTAATCAT 117
Db 464 GCAGGCGATCAAGCTTGGATTTCTATAGTGTACCTAAATTCGAGCTTGGCGTAATCAT 523
QY 118 GGTATAGCTGTTTCTGTGTGAATTTGTTATCGCTCAGATTCACACAAACATACGAG 177
Db 524 GGTATAGCTGTTTCTGTGTGAATTTGTTATCGCTCAGATTCACACAAACATACGAG 583
QY 178 CCGGAAGCATAAAGTGTAAAGCTGGGTGCTTAATGAGTGTAGTCACTCAATTAATG 237
Db 584 CCGGAAGCATAAAGTGTAAAGCTGGGTGCTTAATGAGTGTAGTCACTCAATTAATG 643
QY 238 CGTTGCGCTCACTGCCGCTTTCAGTTCGGGAACCTGTGTCGACCTGCATTAAATGA 297
Db 644 CGTTGCGCTCACTGCCGCTTTCAGTTCGGGAACCTGTGTCGACCTGCATTAAATGA 703
QY 298 TCGGCGCAACCGCGGGAGAGCGGTTTTCGCTATTTGGCGCTCTTCGCTTCCTCGCTCA 357
Db 704 TCGGCGCAACCGCGGGAGAGCGGTTTTCGCTATTTGGCGCTCTTCGCTTCCTCGCTCA 763
QY 358 CTGACTTCGCTCGCTCGCTGCTGCTGCTGCGGAGCGGTATCAGCTCACTCAAAAGCGG 417
Db 764 CTGACTTCGCTCGCTCGCTGCTGCTGCTGCGGAGCGGTATCAGCTCACTCAAAAGCGG 823
QY 418 TAATAGGTTATCCACAGATTCAGGGGATACGCGAGGAAGAAACATGTGAGCAAAAGGCC 477
Db 824 TAATAGGTTATCCACAGATTCAGGGGATACGCGAGGAAGAAACATGTGAGCAAAAGGCC 883
QY 478 AGCAAAAGGCCAGGAACCGCTAAAGAGCGGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTG 537
Db 884 AGCAAAAGGCCAGGAACCGCTAAAGAGCGGCTTTCGCTGCTGCTGCTGCTGCTGCTGCT 943
QY 538 CCCTGACGAGCATCAAAAATTCAGCTCAAGTTCAGGTCAGGTCGGGAACCCGACAGGAC 597
Db 944 CCCTGACGAGCATCAAAAATTCAGGTCAGGTCAGGTCGGGAACCCGACAGGAC 1003
QY 598 TATAAAGATACAGGCGGTTTCCCGCTTGAAGCTCCCTGTCGCTGCTGCTGCTGCTGCTGCTG 657
Db 1004 TATAAAGATACAGGCGGTTTCCCGCTTGAAGCTCCCTGTCGCTGCTGCTGCTGCTGCTGCTG 1063
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QY 658 TGGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGTTTCTCATTA 717
Db 1064 TGGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGTTTCTCATTA 1123
QY 718 GCTCAGCTGTAGGTATCTCA 738
Db 1124 GCTCAGCTGTAGGTATCTCA 1144

RESULT 8
SYNBLM13MV 3204 bp DNA circular SYN 26-JUL-1993
LOCUS
DEFINITION Bluescribe M13 Minus cloning vector.
ACCESSION L08782
VERSION L08782.1 GI:310730
KEYWORDS Synthetic construct DNA.
SOURCE synthetic construct
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 3204)
AUTHORS Gilbert,W.
TITLE Obtained from VecBase 3.0
JOURNAL Unpublished (1991)
COMMENT These data and their annotation were supplied to GenBank by Will
Gilbert under the auspices of the GenBank Curator Program.
Bluescribe M13 Minus - Cloning vector #TYPE DNA CIRCULAR TITLE Bluescribe
ENTRY BLUEM13M
M13 Minus - Cloning vector
DATE 27-MAR-1986
#sequence 16-DEC-1986
#sequence 04-MAR-1987
ACCESSION VB0043
SOURCE artificial
REFERENCE
#number 1
#authors Fernandez J.M., Short J.M., Renshaw M., Huse W., Sorge
J.
#Journal Gene (1987) in press
#citation Sequence data from Stratagene
#comment Sequence correction according to Stratagene COMMENT
Obtained 28-JAN-1987 from Stratagene on floppy disc.
Revised 2-FEB-1986 by F. Pfeiffer:
1580/1 'AT' to 'TA' to match revised sequence of pBR322
Revised 4-MAR-1987 to match sequence of pUC19 on request
of Stratagene
COMMENT
The stand shown corresponds to pUC19c.
As in the published sequence of pUC19c, The M13mp19 lacZ region
is on the complementary strand.
COMMENT
Despite its name Blue M13 minus, this vector contains the
phage fl origin so that the minus strand can be obtained upon
phage fl superinfection.
KEYWORDS
CROSSREFERENCE
#parent
VecBase(3):Blue
#parent
VecBase(3):pUC19, VecSource(3):PromT7, VecSource(3):PromT3,
GenBank(50):PFI
#brother
VecBase(3):BlueM13p
#offspring
VecBase(3):BlueKSm, VecBase(3):BlueSKm
PARENT
Features of BlueM13m (3204 bp)
residue source
1- 238 684- 447 (c) pUC19
239- 694 5488-5943 (c) phage fl
695- 858 448- 285 (c) pUC19
860- 879 1- 20 T7 promoter
881- 937 57- 1 (c) M13mp19/pUC19-polylinker
```


943- 962 20- 1 (c) T3 promoter
966-1202 237- 1 (c) pUC19
1203-3204 2686- 685 (c) pUC19
Conflict (cfl) and Mutations (mut): none
PARENT

Features of BlueM13m (3204 bp)

residue source
1- 238 pUC19c
239- 694 5488-5943 phage f1
695- 853 237- 395 pUC19c
860- 879 1- 20 T7 promoter
881- 937 57- 1 (c) M13mp19/pUC19-polylinker
943- 962 20- 1 (c) T3 promoter
971-3204 453-2686 pUC19c
Conflict (cfl) and Mutations (mut): none
FEATURE

2147-2935 789-1 (c) Ap-R; b-lactamase
POLYLINKER HindIII-SphI-PstI-SalI-XbaI-BamHI-SmaI-KpnI-SacI-EcoRI
SELECTION

#resistance Ap
#indicator beta-galactosidase
SUMMARY BlueM13m #length 3204 #checksum 257.
Location/Qualifiers
1. 3204
/organism="synthetic construct"
/db_xref="taxon:32630"

FEATURES
source

BASE COUNT 776 a 808 c 802 g 818 t
ORIGIN

Query Match 95.6%; Score 705.8; DB 12; Length 3204;
Best Local Similarity 98.0%; Pred. No. 1.2e-188;
Matches 726; Conservative 0; Mismatches 12; Indels 3; Gaps 1;

Oy 1 ATACGACTCACTATAGCGCAATTCAGCTCGGTACCCGGGATCCTCTAGAGTCGACCT 60
Db 862 ATACGACTCACTATAGCGCAATTCAGCTCGGTACCCGGGATCCTCTAGAGTCGACCT 921
Oy 61 GCAGGCATCGAAGCTTGAGTATCTATAGTGCACCTAAAT---AGCTTGGCGTAATCAT 117
Db 922 GCAGGCATCGAAGCTTGAGTATCTATAGTGCACCTAAAT---AGCTTGGCGTAATCAT 981
Oy 118 GGTATAGCTGTTTCTGCTGTAATTTATCCGCTCACAAATCCACAAATACGAG 177
Db 982 GGTATAGCTGTTTCTGCTGTAATTTATCCGCTCACAAATCCACAAATACGAG 1041
Oy 178 CCGGAACATAAAGTGTAAAGCTTGGGTCCTAATAGTGAGCTAACATCAATTAATTG 237
Db 1042 CCGGAACATAAAGTGTAAAGCTTGGGTCCTAATAGTGAGCTAACATCAATTAATTG 1101
Oy 238 CGTTGCGCTCACTGCGCGCTTCCAGTCGGGAACCTGCTGCGAGCTGCATTAATCAA 297
Db 1102 CGTTGCGCTCACTGCGCGCTTCCAGTCGGGAACCTGCTGCGAGCTGCATTAATCAA 1161
Oy 298 TCGGCCAACCGCGGGAGAGCGGTTTGGCTATTTGGCGCTCTTCGCTTCCTCGCTCA 357
Db 1162 TCGGCCAACCGCGGGAGAGCGGTTTGGCTATTTGGCGCTCTTCGCTTCCTCGCTCA 1221
Oy 358 CTGACTCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 417
Db 1222 CTGACTCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1281
Oy 418 TAATACGGTTATCCACAGAAATCAGGGGATACGAGGAAAGAAATGTAGCAAAAGGCC 477
Db 1282 TAATACGGTTATCCACAGAAATCAGGGGATACGAGGAAAGAAATGTAGCAAAAGGCC 1341
Oy 478 AGCAAAAGCCAGGAAACCGTAAAGGCGCGGTTGCTGGCGTTTTCATAGGCTCCGCC 537
Db 1342 AGCAAAAGCCAGGAAACCGTAAAGGCGCGGTTGCTGGCGTTTTCATAGGCTCCGCC 1401
Oy 538 CCCTGACGAGCATCACAAATACGAGCTCAAGTCAGAGTGGCGAAACCCGACAGGAC 597
Db 1402 CCCTGACGAGCATCACAAATACGAGCTCAAGTCAGAGTGGCGAAACCCGACAGGAC 1461

Oy 598 TATAAAGATACCAAGGCTTTCCCTCGGAAGTCCCTCGTGGGCTCTCTCTGTCGAGCC 657
Db 1462 TATAAAGATACCAAGGCTTTCCCTCGGAAGTCCCTCGTGGGCTCTCTCTGTCGAGCC 1521
Oy 658 TGCGGCTTACCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCTATA 717
Db 1522 TGCGGCTTACCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCTATA 1581
Oy 718 GCTCAGCTCTAGGTATCTCA 738
Db 1582 GCTCAGCTCTAGGTATCTCA 1602

RESULT 9
SYNBLM13PV
LOCUS BlueM13PV 3204 bp DNA circular SYN 26-JUL-1993
DEFINITION Bluescribe M13 Plus cloning vector.
ACCESSION L08783
VERSION L08783.1 GI:310731
KEYWORDS Synthetic construct DNA.
SOURCE synthetic construct
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 3204)
AUTHORS Gilbert, W.
TITLE Obtained from VecBase 3.0
JOURNAL Unpublished (1991)
COMMENT These data and their annotation were supplied to GenBank by Will Gilbert under the auspices of the GenBank Curator Program.
BlueScribe M13 Plus - Cloning vector
ENTRY BLUEM13P
M13 Plus - Cloning vector #TYPE DNA CIRCULAR TITLE BlueScribe

DATE 27-MAR-1986
#sequence 16-DEC-1986
ACCESSION VB0044
SOURCE artificial
REFERENCE
#number 1
#authors Fernandez J.M., Short J.M., Renshaw M., Huse W., Sorge J.

#journal Gene (1987) in press
#citation Sequence data from Stratagene
#comment sequence correction according to Stratagene
Obtained 28-JAN-1987 from Stratagene on floppy disc.
Revised 2-FEB-1986 by F. Pfeiffer:
1580/1 'AT' to 'TA' to match revised sequence of pBR322
Revised 4-MAR-1987 to match sequence of pUC19 on request
of Stratagene

COMMENT
The stand shown corresponds to pUC19c.
As in the published sequence of pUC19c, The M13mp19 lacZ region
is on the complementary strand.

COMMENT
Despite its name Blue M13 plus, this vector contains the
phage f1 origin so that the plus strand can be obtained upon
phage f1 superinfection.

KEYWORDS
CROSSREFERENCE
#parent
VecBase(3):Blue
#parent
VecBase(3):pUC19, VecSource(3):PromT7, VecSource(3):PromT3,
GenBank(50):PFI
#brother
VecBase(3):BlueM13m
#offspring
VecBase(3):BlueKsp, VecBase(3):BluesKp

PARENT
Features of BlueM13p (3204 bp)
residue source
1- 238 684- 447 (c) pUC19

1	ATACGACTCACTATAGGCGGAATTCGAGCTCGGTACCCGGGATCCTCTAGAGTCGACCT	60
686	ATAGGACTCACTATAGGCGGAATTCGAGCTCGGTACCCGGGATCCTCTAGAGTCGAAG	745
61	GCAGGC-----ATCCAGCTTTGAGTATTCATAGTGTCACTTAATATAG	103
746	CTTCTCGCCCTATAGTCAGTCGTATTTACAGCTTTGAGTATTCATAGTGTCACTTAATATAG	805
104	CTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAATTTATCCGCTCACAATTC	163
806	CTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAATTTATCCGCTCACAATTC	865
164	ACACAACATACGAGCGCGAAGCATAAAGGTAAAGCCGTGGGTGCCCTTAATCAGTGA	223
866	ACACAACATACGAGCGCGAAGCATAAAGGTAAAGCCGTGGGTGCCCTTAATCAGTGA	925
224	ACTCACATTAATTCGGCTTGGGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTCGTGCCA	283

BASE COUNT
ORIGIN

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2268 a 1705 c 1858 g 2295 t
/note="Sphi restriction site"

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Query Match 93.4%; Score 689.4; DB 6; Length 8126;
 Best Local Similarity 99.9%; Pred. No. 5.4e-184;
 Matches 690; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 48 CTAGAGTGCACCTCGAGGATGCAAGCTTCAGTATCTATAGTGTCCACCTAATAGCTTG 107
 DB 4956 CTAGAGTGCACCTCGAGGATGCAAGCTTCAGTATCTATAGTGTCCACCTAATAGCTTG 5015
 QY 108 GCGTAATCATGTCATAGCTGTTTCCTGCTGTAATGTTATCCCGCTCAAAATTCACAC 167
 DB 5016 GCGTAATCATGTCATAGCTGTTTCCTGCTGTAATGTTATCCCGCTCAAAATTCACAC 5075
 QY 168 RACATACGAGCGGAGCATAAAGCTTAAGCTGCGGCTGCTTAATGAGTGAGCTAACTC 227
 DB 5076 RACATACGAGCGGAGCATAAAGCTTAAGCTGCGGCTGCTTAATGAGTGAGCTAACTC 5135
 QY 228 ACATTAATTCGCTGCGCTCACTGCCGCTTCCAGTCGGGAAACCTGTCGTCGACGCTG 287
 DB 5136 ACATTAATTCGCTGCGCTCACTGCCGCTTCCAGTCGGGAAACCTGTCGTCGACGCTG 5195
 QY 288 CATTAAATCAATCGGCAACGCGGAGAGGCGGTTTGGCTATTGGGCGCTTCCGCT 347
 DB 5196 CATTAAATCAATCGGCAACGCGGAGAGGCGGTTTGGCTATTGGGCGCTTCCGCT 5255
 QY 348 TCCTCGCTCACTGACTCGCTCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 407
 DB 5256 TCCTCGCTCACTGACTCGCTCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5315
 QY 408 TCAAAAGGCGGTAATACGTTATCCACAGAAATACAGGGGATAACGAGGAAAGACATGTGA 467
 DB 5316 TCAAAAGGCGGTAATACGTTATCCACAGAAATACAGGGGATAACGAGGAAAGACATGTGA 5375
 QY 468 GCAAAAGGCGGCAAAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 527
 DB 5376 GCAAAAGGCGGCAAAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5435
 QY 528 AGGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 587
 DB 5436 AGGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 5495
 QY 588 CCGACAGGACTATAAGATACAGGCGGTTTCCCGCTCGAGAGCTCCCTCGGCGCTGCT 647
 DB 5496 CCGACAGGACTATAAGATACAGGCGGTTTCCCGCTCGAGAGCTCCCTCGGCGCTGCT 5555
 QY 648 GTTCGACCGCTCGGCTTACCGGATACCTGTCGCGCTTCTCCCTTGGGAAAGCGTGGCG 707
 DB 5556 GTTCGACCGCTCGGCTTACCGGATACCTGTCGCGCTTCTCCCTTGGGAAAGCGTGGCG 5615
 QY 708 CTTTCTCATAGCTACGCTGAGTATCTCA 738
 DB 5616 CTTTCTCATAGCTACGCTGAGTATCTCA 5646

RESULT 13
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 LOCUS CVPGEN4Z 2746 bp DNA circular SYN 26-JAN-2000
 DEFINITION Cloning vector pGEM-4Z.
 ACCESSION X65305
 VERSION X65305.2 GI:6782314
 KEYWORDS beta-lactamase; bla gene; cloning vector; lacZ gene; multiple cloning site; promoter.
 SOURCE Cloning vector pGEM-4Z.
 ORGANISM artificial sequence; vectors.
 REFERENCE 1 (bases 1 to 2746)
 AUTHORS Technical Services.
 TITLE Direct Submission
 JOURNAL Submitted (23-MAR-1992) Technical Services, Promega Corporation, 2800 Woods Hollow Road, Madison, WI 53711-5399, USA
 REMARK revised by [2]
 REFERENCE 2 (bases 1 to 2746)

AUTHORS Technical Services.
 TITLE Direct Submission
 JOURNAL Submitted (28-MAY-1993) Technical Services, Promega Corporation, 2800 Woods Hollow Road, Madison, WI 53711-5399, USA
 REMARK revised by [3]
 REFERENCE 3 (bases 1 to 2746)
 AUTHORS Technical Services.
 TITLE Direct Submission
 JOURNAL Submitted (26-JAN-2000) Technical Services, Promega Corporation, 2800 Woods Hollow Road, Madison, WI 53711-5399, USA
 COMMENT On Jan 27, 2000 this sequence version replaced
 See X65300-X65335 for related vector sequences
 This vector can be obtained from Promega Corporation, Madison, WI.
 Call one of the following numbers for order or technical information:
 Order or Technical 800-356-9526
 In Wisconsin 800-356-9526
 Outside U.S. 608-274-4330.

FEATURES
 source location/Qualifiers
 1..2746
 /organism="Cloning vector pGEM-4Z"
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 7..63
 misc_feature /note="multiple cloning sites"
 68..87
 promoter /note="T7 promoter"
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 96..325
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 complement(106..122)
 primer_bind /note="pUC/M13 reverse sequencing primer"
 complement(108..110)
 gene /gene="lacZ"
 complement(108..110)
 misc_feature /gene="lacZ"
 complement(108..110)
 /note="lacZ start codon"
 130..146
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 complement(1267..2127)
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 DRPELNEAIPIQNDERTMPVAMATLTKLLTGLLTLASRQOLIDWMEADKVGPL
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 2563..2726
 misc_feature /note="lac operon sequence"
 2686..2702
 primer_bind /note="pUC/M13 forward sequencing primer"
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 promoter /note="SP6 promoter"
 679 t
 BASE COUNT 684 a 684 c 699 g 679 t
 ORIGIN

Query Match 92.8%; Score 684.8; DB 12; Length 2746;
 Best Local Similarity 96.9%; Pred. No. 1.1e-182;
 Matches 698; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 19 CCAATTCAGCTCGGTACCCGGGATCCTTAGAGTCGACCTCGACGATGCAAGCTTGA 78
 DB 6 CCAATTCAGCTCGGTACCCGGGATCCTTAGAGTCGACCTCGACGATGCAAGCTTGT 65


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QY 497 TAAAAAGCCGCGTTCGTCGGCTTTTCCATAGGCTCCGCCCTCGAGGACATCAAA 556
Db 1352 TAAAAAGCCGCGTTCGTCGGCTTTTTCGATAGGCTCCGCCCTCGAGGACATCAAA 1411
QY 557 AAATCGACGCTCAAGTCAGAGTGGCGAAACCCGACAGACTATAAAGATACCAAGCGCTT 616
Db 1412 AAATCGACGCTCAAGTCAGAGTGGCGAAACCCGACAGACTATAAAGATACCAAGCGCTT 1471
QY 617 TCCCCCTGGAGCTCCCTCGTCGGCTTCCTGTCGACCCCTGCCGCTTACCGGATACCT 676
Db 1472 TCCCCCTGGAGCTCCCTCGTCGGCTTCCTGTCGACCCCTGCCGCTTACCGGATACCT 1531
QY 677 GTCCGCGCTTTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCT 736
Db 1532 GTCCGCGCTTTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCT 1591
QY 737 CA 738
Db 1592 CA 1593

RESULT 15
AF134573
LOCUS AF134573 3946 bp DNA linear SYN 03-MAY-1999
DEFINITION Cloning vector p34S-Sm3, complete sequence.
ACCESSION AF134573
VERSION AF134573.1 GI:4731624
KEYWORDS Cloning vector p34S-Sm3.
SOURCE Cloning vector p34S-Sm3
ORGANISM artificial sequence; vectors.
REFERENCE 1 (bases 1 to 3946)
AUTHORS Dennis,J.J. and Zylstra,G.J.
TITLE Construction of a modified Sm/Sp resistance cassette
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3946)
AUTHORS Dennis,J.J. and Zylstra,G.J.
TITLE Direct Submission
JOURNAL Submitted (12-MAR-1999) Biotechnology Center for Agriculture and the Environment, Cook College, Rutgers University, 59 Dudley Rd., New Brunswick, NJ 08901-8520, USA
FEATURES
source 1..3946
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/db_xref="taxon:92792"
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misc_feature 1..51
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1210..1260
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complement(2464..3324)
/gene="bla"
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/protein_id="AAD28533.1"

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DRWPELNEATIPNDERPTTMPVAMPTTLRLKLITGELLTLASRQLLDNMEADKVAQPL
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EIGASLIKHW"
BASE COUNT 971 a 983 c 1047 g 945 t
ORIGIN

Query Match 92.0%; Score 679; DB 12; Length 3946;
Best Local Similarity 95.9%; Pred. No. 4.7e-181;
Matches 697; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 12 TATAGGGCGAATTCAGCTCGGTACCCCGGGGATCCTCTAGAGTCGACCTCGAGGACATGCA 71
Db 1196 TATCGGCAATTAAGAGCTCGGTACCCCGGGATCCTCTAGAGTCGACCTCGAGGACATGCA 1255
QY 72 AGCTTGAGTATTCTATAGTGTACCTAAATAGCTTGGCGTAATCATGTCATATAGCTGTTT 131
Db 1256 AGCTTGCTCCCTATAGTGTAGTTCGTTAGAGCTTGGCGTAATCATGTCATAGCTGTTT 1315
QY 132 CCTGTGTGAATTTGTTATCCGCTCACAATTCACACAAACATACGAGCCGGAAGCATAAAG 191
Db 1316 CCTGTGTGAATTTGTTATCCGCTCACAATTCACACAAACATACGAGCCGGAAGCATAAAG 1375
QY 192 TGTAAAGCCTGGGGTGCCTTAATGAGTGAGCTAACTACATTAATTCGTTGCGCTCACTG 251
Db 1376 TGTAAAGCCTGGGGTGCCTTAATGAGTGAGCTAACTACATTAATTCGTTGCGCTCACTG 1435
QY 252 CCGCGTTTCCAGTCGCGGAACCTGCTGCCAGCTGCATTAATGAATCGCCCAACGGCGG 311
Db 1436 CCGCGTTTCCAGTCGCGGAACCTGCTGCCAGCTGCATTAATGAATCGCCCAACGGCGG 1495
QY 312 GGGAGAGCGGTTTCGCTATTGGCGCTCTTCCGCTTCCCTCGCTCACTGACTGCTGCTGCGC 371
Db 1496 GGGAGAGCGGTTTCGCTATTGGCGCTCTTCCGCTTCCCTCGCTCACTGACTGCTGCTGCGC 1555
QY 372 TCGGTGCTTCCGCTCGCGGAGCGGTATCAGCTCACTCAAGGGGGTAATACGGTTATCC 431
Db 1556 TCGGTGCTTCCGCTCGCGGAGCGGTATCAGCTCACTCAAGGGGGTAATACGGTTATCC 1615
QY 432 ACAGAAATCAGGGGATACGACAGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGG 491
Db 1616 ACAGAAATCAGGGGATACGACAGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGG 1675
QY 492 AACCGTAAAGAGCCGCTGCTGCGCTTTTCCATAGGCTCGCGCCCTCGAGGACAT 551
Db 1676 AACCGTAAAGAGCCGCTGCTGCGCTTTTCCATAGGCTCGCGCCCTCGAGGACAT 1735
QY 552 CACAAAAATTCAGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACCAG 611
Db 1736 CACAAAAATTCAGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACCAG 1795
QY 612 GCGTTTCCCGCTGGAAGCTCCCTCGTCGGCTCTCTGTCGACCGCTGCCGCTTACCGGA 671
Db 1796 GCGTTTCCCGCTGGAAGCTCCCTCGTCGGCTCTCTGTCGACCGCTGCCGCTTACCGGA 1855
QY 672 TACCTGTCCGCTTTCTCCCTTCGCGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGG 731
Db 1856 TACCTGTCCGCTTTCTCCCTTCGCGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGG 1915
QY 732 TATCTCA 738
Db 1916 TATCTCA 1922

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 09:37:28 ; Search time 365.16 Seconds
(without alignments)
3469.939 Million cell updates/sec

Title: US-10-014-743-3
Perfect score: 738
Sequence: 1 ATACGACTCACTATAGGCG.....CTCAGCGTGTAGGTATCTCA 738

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N.Geneseq_0328021.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	738	100.0	738	20	AAZ09716
2	723	98.0	972	21	AAZ09716
3	723	98.0	3253	19	AAV43439
4	691.8	93.7	3216	22	AAZ09993
5	691.8	93.7	3216	22	AAZ09993
6	689.4	93.4	8126	18	AAZ29606
7	672.4	91.1	4283	18	AAZ86449
8	672.4	91.1	4283	19	AAZ86610
9	672.4	91.1	4283	21	AAA63237

10	569	90.7	4118	18	AAZ09188	Construct pGEM-htr
11	569	90.7	4118	18	AAZ09189	Construct pGEM-htr
12	667.8	90.5	4539	16	AAZ07347	Plasmid pINVI. SY
13	667.8	90.5	4539	19	AAV37292	Plasmid pINVI used
C 14	667	90.4	2571	21	AAZ62824	Glyceraldehyde-3-p
C 15	667	90.4	2571	24	AAK17089	Eucaalyptus grandis
C 16	667	90.4	3018	20	AAZ29905	Plasmid pGEM (RTM)
17	667	90.4	3968	22	AAZ09981	PHSP70-1MCS constr
18	667	90.4	4229	22	AAZ09981	Genetic informatio
19	667	90.4	4626	22	AAZ09988	PHSP-ohoxDS/BH pla
20	667	90.4	5919	22	AAZ09988	PHSP-GUS construct
21	667	90.4	7175	21	AAZ09988	Plasmid pGALIPNIST
22	667	90.4	7177	21	AAZ09989	Plasmid pGALIPNIST
23	666.8	90.4	10930	16	AAQ81226	Plasmid pM16-1. C
24	666.8	90.4	10950	16	AAQ81225	Plasmid pM16. Chi
25	666	90.2	4454	22	AAZ06386	Vector pGX104 DNA
26	666	90.2	4620	22	AAZ06383	Vector pGX8 DNA se
27	666	90.2	4643	22	AAZ06385	Vector pGX52 DNA s
28	666	90.2	4701	22	AAZ06387	Vector pGX18 DNA s
29	666	90.2	4756	22	AAZ06384	Vector pGX22 DNA s
30	665.8	90.2	6688	22	AAZ08333	Plasmid pAN336 for
C 31	665.4	90.2	5115	20	AAZ08719	Chimeric gene cons
32	665.4	90.2	8320	22	AAZ02322	Plasmid pAN296 for
33	665.4	90.2	8803	22	AAZ02321	Plasmid pAN294 for
34	665.4	90.2	13928	22	AAH77500	Haemophilia B gene
C 35	660.4	89.5	10306	15	AAZ07374	Retro virus vector
C 36	660.4	89.5	10970	15	AAZ07375	Retro virus vector
C 37	659.4	89.3	9837	18	AAZ06851	Intron 21 of human
C 38	650.8	88.2	4161	24	ABA04699	Plasmid pB5/35Sbar
39	650.4	88.1	742	22	AAH82483	Human ovarian tumo
40	644.6	87.3	3854	15	AAQ67221	Plasmid pSEC-cyt/c
C 41	642.4	87.0	4344	21	AAZ53848	Vector pTGF67. S
C 42	642.4	87.0	4344	21	AAZ53835	Vector pTGF67. S
C 43	642.4	87.0	5753	22	AAZ18173	Vector pTGF67. S
C 44	642.4	87.0	5753	22	AAZ18173	Human wild-type fa
C 45	642.4	87.0	10698	22	AAZ18172	Human factor VIII
						Human factor VIII

ALIGNMENTS

RESULT 1
AAZ09716
ID AAZ09716 standard; DNA; 738 BP.

AC AAZ09716:

DT 15-NOV-1999 (first entry)

DE Plasmid pGEM DNA fragment.

XX Energy transfer dye; fluorescence; donor: acceptor; excitation energy;

XX Light absorbition; nucleic acid sequencing; detection; fluorophore; ss.

XX Synthetic.

XX US5945526-A.

XX 31-AUG-1999.

XX 23-MAR-1998; 98US-0046203.

XX 23-MAR-1998; 98US-0046203.

PR 03-MAY-1996; 96US-0642330.

PR 27-JUN-1996; 96US-0672196.

PA (PEKE) PERKIN-ELMER CORP.

PI Lee LG, Rosenblum B, Spurgeon SL;

DR WPI, 1999-550120/46.

XX New energy transfer dye, used in nucleic acid sequencing

XX PS

Disclosure; Column 87-90; 77pp; English.

This invention describes a novel energy transfer dye (1) which comprises a donor dye which is capable of absorbing light at a first wavelength and emitting excitation energy in response, and an acceptor dye which is capable of absorbing the excitation energy emitted by the donor and fluorescing at a second wavelength. (1) are used in processes for sequencing nucleic acids. (1) can be used in a wide variety of methods for detecting the presence of a component in a sample by labeling the component with (1). They are especially useful in processes which combine separation with fluorescent detection techniques, particularly methods requiring the simultaneous detection of multiple spatially overlapping analytes. (1) have a strong fluorescent signal, the orientation between the donor and acceptor fluorophores is such that the energy is efficiently transferred between them. This sequence represents a fragment of plasmid pGEM DNA which is used to describe the method of the invention.

Sequence 738 BP; 170 A; 208 C; 192 G; 168 T; 0 other:

```

Query Match      100.0%; Score 738; DB 20; Length 738;
Best Local Similarity 100.0%; Pred. No. 1.6e-124;
Matches 738; Conservative 0; Mismatches 0; Indels 0

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1	atacgactcactatagggcggaattcgagctcggtatcccggggatactctctagagtcgacct	60	Db
61	CGAGCATGCAAGCTTGAGTATTCTATAGTGTGCACCTAAATAGCTTGGCGTAAATCATGGT	120	QY
61	gcaggcatcgaaagcttgagttattctatagtgtaacctaaatagcttggcgttaatacattg	120	Db
121	CATAGCTGTTTCTGTGTGAATATGTTATTCGCTCACAAATTCACACAAATACGAGCCG	180	QY
121	catagctgtttctctgttgaaattgttaacctcaaatctccacacaatacagagcog	180	Db
191	GAAGCATAAAGTGTAAAGCCTGGGGTCCCTAATGAGTGAGCTAACTCACATTAAATTCGGT	240	QY
191	gaagcataaagtgtaagcctggggtgcctaaatgagtagagctaactcacataatttcgct	240	Db
241	TGCCTCCTACCTGCSCGCTTTCACAGTCGGGAACCTGCTGTCACAGCTCATTAATGAATCG	300	QY
241	tgcctcactgcscgctttccagtcggtggaacctgctggtccagctgcattaatgaatcg	300	Db
301	GCCAAACGCGGGGAGAGCGGTTTGCCTATTGGCGCTCTTCGCGTCTCTCGCTCACATG	360	QY
301	gcaaacgcgcggggagagcggtttgcgtattggcgctcttcgcgttctctcgctcaactg	360	Db
361	ACTCGCTGCCTCGGTGCTTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAGAGCGGTAA	420	QY
361	actcgcctgcctcgggtcgcttcgctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	420	Db
421	TACGTTTATCCACAGAAATCAGGGGATACGCAGAGAAAGAACATCTGAGCAAAAGCCACG	480	QY
421	tacggttatccaagaaatcaggggataacgcaggaaagaacatgtgagcaaaaggccagc	480	Db
481	AAAAGGCCAGGAACCGTAAAAAGGCGCGGTTGCTGGCGTATTTCCATAGGCTCGCGCCCG	540	QY
481	aaaaggccaggaaccgcataaaaggccgcgttgcctggcggttttcccataggtctcgcgcgc	540	Db
541	CTGACGAGCATCACAAAAATCAGACGCTCAAGTCAAGAGGTGGCGAAACCCGACAGGACTAT	600	QY
541	ctgacgagcatcacaataatcagcgtcgaagtcagaggttgcgaaaccgcagagactat	600	Db
601	AAAGATACCAAGGCGTTTCCCTCGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCCTCG	660	QY
601	aaagataccaagcggtttcccccctggaaagctcccctgcctctctctctgttcgcgaacctgc	660	Db
661	CGCTTACCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCTAGCT	720	QY
661	cgtctaccggatactcgtccgccttctcccttcgcgggaagcgttggcgtcttctctcatagct	720	Db

PI Plaetinck G, Mortier K, Lissens A, Bogaert T;
XX WPI; 2001-425660/45.
XX Inhibiting target gene expression in nematode worm by feeding it a food
XX organism capable of producing double-stranded RNA structure having a
XX sequence identical to target gene following ingestion of the food -
XX Example 1; Page 50-51; 60pp; English.
XX The present sequence for vector pGNI comprises opposable
XX bacteriophage T7 promoters flanking a multiple cloning site and
XX an ampicillin resistance marker. The sequence is described in an
XX invention relating to a method of inhibiting expression of a target
XX gene in a nematode worm (e.g. *Caenorhabditis elegans*). The method
XX involves feeding to the worm a food organism which is capable of
XX producing a double-stranded RNA structure having a nucleotide sequence
XX substantially identical to a portion of the target gene following
XX ingestion of the food organism by the nematode, or by introducing a DNA
XX capable of producing the double-stranded RNA structure. The nematode
XX worm has a non wild-type genetic background selected to provide
XX increased sensitivity to RNA interference as compared to wild type,
XX and exhibits increased gut uptake compared to wild type.
XX SQ Sequence 3216 BP; 827 A; 788 C; 821 G; 780 T; 0 other;
Query Match 93.7%; Score 691.8; DB 22; Length 3216;
Best Local Similarity 96.2%; Pred No. 2.6e-116;
Matches 726; Conservative 0; Mismatches 12; Indels 17; Gaps 1;
QY 1 ATAGACTCACTATAGGGCGAATCGAGTCGGTACCGGGGATCCCTCTAGATCGACCT 60
Db 686 atagactcactatagggcgaaatcgagtcggtagccgggagatccctctagatcgaaag 745
QY 61 GCAGGC-----ATCGAAGCTTGAGTATTCTATAGTGTCACTCAATAATAG 103
Db 746 ctctcgccctatagtagtcgtatatacagcttgatgtatctatagtcacctaataag 805
QY 104 CTTGCGGPAATCATGTCATAGCTGTTTCTGTGTGAATTTATCCGCTCACAATTC 163
Db 806 cttagcgttaactagtcgtatagctgttctgtgaaattgtatccgcgcacaatttc 865
QY 164 ACACAACTACGACGCGAAGCATAAAGTGTAAAGCTGGGCTGCCTAATGAGTAGCTA 223
Db 866 acacaacatacgagccggaagcataaagtgtaaagcctgggtgcctaagttagtgagcta 925
QY 224 ACTCATTAATTTGGTTCGCTCACTGCGGCTTCCAGTCGGGAAACCTGTCTGCGCA 283
Db 926 actcataaattggttgcgtcactgcccgccttccagtcggygaaacctgctgcca 985
QY 284 GCTGATTAAATGATCGGCCAACCGCGGGGAGAGCGGTTTGGTATTGGCGCTCTTC 343
Db 986 gctgcattaataatcgcccaacgcgcggagagcggtttgctgattggcgctcttc 1045
QY 344 CGCTTCCTCGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 403
Db 1046 cgtctctcgcctcactgactcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 1105
QY 404 TCACCTCAAAAGCGGTAATACGGTTATCCACAGATACAGGGGATACGCGAGGAACAT 463
Db 1106 tcactcaaggcggtaataacggttatccacagatcaggggatacgcagggaaagaaat 1165
QY 464 GTGAGCAAAAGCCAGCAAAAGGCGCAGGACCGGTAAAGGCGCGTTCGTCGCTTTT 523
Db 1166 gtgagcaaaaggccagcaaaaggccaggaacccgtaaaaggccgcgttctgctgctttt 1225
QY 524 CCATAGGCTCGCGCCCTGACGACATCACAATAATCGACGCTCAAGTCAGAGGTGGGG 583
Db 1226 cgaataggtctccgccccctgacgagcaacacaaaaacgacgctcagagcagggcggc 1285
QY 584 AAACCCGACAGGACTATAAGATACAGGCGTTTCCCGCTGGAGCTCCCTGCTGGGCTTC 643
Db 1286 aaacccgacagactataagatatacagcggtttcccccctggaaagctccctcgtgcgctc 1345
QY 644 TCCTGTTTCGACCCCTGCGGCTTACCGATACCTGTCGGCTTTCCTCCCTGCGGAGCGT 703
Db 1346 tccgtttccgacctgcgcgttacccgataccgcttccttcctcccttcgggaagcgt 1405
QY 704 GCGGCTTTCCTATAGCTACAGCTGCTGAGTATCTCA 738
Db 1406 ggcgtttctctatagctcacgctgtaggtatctca 1440

RESULT 6
AAZ29606
ID AAZ29606 standard; DNA; 8126 BP.
XX AAZ29606;
AC AAZ29606;
XX 30-MAR-2000 (first entry)
XX Basic fragmentation vector, pDVO DNA.
XX Fragmentation vector; pDVO DNA; target sequence; triplet repeat; yeast;
XX lysine-2 gene; selectable marker; Yeast Artificial Chromosome; YAC;
XX telomere; homologous recombination; deletion fragment; sequencing;
XX End Rescue Site; ERS; positional information; contig mapping; ds.
XX Saccharomyces cerevisiae.
OS Synthetic.
XX Key Location/Qualifiers
XX misc_feature 1..14
FT /tag= a
FT /label= End_Rescue_Site
FT /note= "Contains restriction sites for EcoRI, BamHI,
FT KpnI and ClaI"
FT mat_peptide 15..4819
FT /tag= b
FT /label= Yeast_Lysine-2_marker
FT /note= "Selection marker"
FT /function= "Used for acentromeric fragmentation"
FT 4820..4961
FT /tag= c
FT /label= Yeast_telomere_sequence
FT /note= "Used for acentromeric fragmentation"
FT 4962..8126
FT /tag= d
FT /label= pGem3zf(-)_vector_sequence
XX WO9966059-A1.
XX 23-DEC-1999.
XX 11-JUN-1999; 99WO-EP04106.
XX 12-JUN-1998; 98EP-0201976.
XX (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX Del-Favero J, Van-Broeckhoven C;
XX WPI; 2000-116773/10.
XX Fragmentation vector for producing deletion fragments of yeast
XX artificial chromosomes for genome mapping -
XX Claim 1; Fig 8; 52pp; English.
XX The present sequence is the basic fragmentation vector DNA, pDVO.
XX The vector comprises a yeast telomere sequence, a selectable marker,
XX yeast Lysine-2 gene and a repetitive element comprising triplet repeat
XX regions, allowing for homologous recombination, between the vector and
XX the YAC. It has Sali restriction site (4961-4966) for linearisation of
XX the vector, PstI site (4967-4972) for cloning of target sequence and

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XX	PN	US5697901-A.			
XX	PD	16-DEC-1997.			
XX	PF	19-MAY-1995; 95US-0445265.			
XX	PR	14-DEC-1989; 89US-0451957.			
XX	PR	22-MAY-1991; 91US-0707248.			
XX	PR	11-JUN-1992; 92US-0897357.			
XX	PR	11-JUN-1993; 93US-0076550.			
XX	PA	(ERIK/) ERIKSSON E.			
XX	PI	Eriksson E;			
XX	XX	WPI; 1998-051325/05.			
DR	DR	P-PSDB; AAW43092.			
XX	XX	Introducing genetic material into tissue cells - by injection with microneedle			
XX	PS	Example 2; Columns 15-20; 21pp; English.			
XX	XX	The present sequence represents epidermal growth factor-encoding plasmid DNA which was used in a new method for introducing genetic material into a cell, comprising repeatedly injecting the genetic material into cells of a target tissue at an in-situ site with a microneedle, whereby a change in the animal attributable to the delivery of the genetic material is detectable. The target tissue is selected from skin cells of a wound, and the target cells may be covered with a protective chamber. The method is used for obtaining long-term expression of native or non-native proteins, e.g. for secretion into the bloodstream or lymphatic system, or for preventing expression of proteins eliciting an immune response.			
XX	SQ	Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;			
Query Match 91.1%; Score 672.4; DB 19; Length 4283;					
Best Local Similarity 99.9%; Pred. No. 7.6e-113;					
Matches 673; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
QY	65	GCATGCAAGCTTACGATTTCTATAGTGTCACTAAATAGCTTGGCGTAAATCATGTGTCATA 124			
DB	1590	gcatagaagcttgatctatctatagtcacactaaatagcttgatgctgaatcatggtcata 1649			
QY	125	GCTGTTTCTGTTGAAATTTTTCCTCACAATCCACACACATACAGCGCGAAG 184			
DB	1650	gctgtttcctgtgaaattgttccctcacaattccacacacatacagacccggaag 1709			
QY	185	CATAAAGCTTAAAGCCTGGGCTGCTTAATGAGTGAGCTCACTCAATTAATTCGTTGGC 244			
DB	1710	cataaagttaaagcctgggtgctgaatgagtgagtaactcacatgaatgaatcgcca 1829			
QY	245	CTCAGTCCCGCTTTCAGTCCGGAACCTGCTGTCGACGCTGCTATTAATGAATCGGCCA 304			
DB	1770	ctcactgcctgttccagttccagtcgggaaccctgctgctgacatgaatgagtcgcca 1889			
QY	305	ACGCGCGGGAGAGCGGTTTTCGTTATTTGGCGCTTTCCTTCCTCGCTCACTGACTC 364			
DB	1830	acgcgcgggagagcggtttgctgattggtggtcttccgcttccctcactgactc 1889			
QY	365	GCTGCGCTGCGTTCGCTGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 424			
DB	1890	gctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 1949			
QY	425	GTTATCCACAGATCAGGGATACGAGGATACGAGGATACGAGGATACGAGGATACGAG 484			
DB	1950	gttatccacagatcaggggataacgcgaggggaaagaaatgtagcaaaagccagcaaa 2009			
QY	485	GGCCAGGAACCGTAAAAAGCGCGGTTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 544			
DB	2010	ggccaggaacccgtaaaaagcgcggttctgctgctgctgctgctgctgctgctgctg 2069			

Db 2250 ctgtagtatctca 2263

RESULT 10
ID AAT69188 standard; DNA; 4118 BP.

XX AC AAT69188;
XX AC AAT69188;
XX DT 26-FEB-1998 (first entry)
XX XX Construct pGEM-hTR containing RNA component of human telomerase.
XX DE Human telomerase; quantification; tumour cell; pGEM-hTR;
XX KW detection; micrometastasis; diagnosis; lymphoblastoma; leukaemia;
XX KW teratocarcinoma; melanoma; carcinoma; cancer; tumour; neuroblastoma;
XX KW rhabdomyosarcoma; leiomyosarcoma; lymphoma; RNA component; ss.
XX XX Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT misc_feature 12..975
XX FT /*tag= a
XX FT /note= "cDNA from RNA component of human telomerase"
XX XX WO9718322-A2.
XX XX 22-MAY-1997.
XX XX 14-NOV-1996; 96WO-DE02183.
XX XX 16-NOV-1995; 95DB-4042795.
XX PA (DAHM/) DAHM M W.
XX PI Dahm MW;
XX XX WPI; 1997-289298/26.
XX XX Quantifying tumour cells in body fluid - by measuring RNA component
XX PT of telomerase after amplification, especially useful for early
XX PT diagnosis of metastasis
XX XX Example 5; Fig 5; 46pp; German.
XX CC The present sequence is the construct pGEM-hTR, which comprises the
XX CC transcription vector pGEM-13zf(+) and the cDNA from the RNA
XX CC component of human telomerase. The construct was used in the
XX CC development of a novel method for quantifying tumour cells in a
XX CC body fluid. The method comprises specific amplification of the RNA
XX CC component of telomerase, and measuring the amount of amplified
XX CC nucleic acid. At least 1, preferably all 3 (AAT69173-75) standard
XX CC co-amplified with telomerase DNA. The amplification products are
XX CC detected directly or via a label or by hybridisation with a
XX CC labelled oligonucleotide (AAT69184-87, 1 for each standard and 1 for
XX CC telomerase), and the amount of telomerase product compared with
XX CC that from the standards.
XX CC The method can be used to detect tumour cells, specifically
XX CC micrometastases, in a body fluid, particularly for the early
XX CC diagnosis of metastatic spread and for monitoring tumour therapy.
XX CC Typical tumour cells that can be quantified are micrometastases,
XX CC T cell lymphoblastoma or leukaemia (chronic myelogenous, and
XX CC chronic or acute lymphatic leukaemia), teratocarcinoma, melanoma,
XX CC carcinoma of lung, liver or prostate, cancer of colon or breast,
XX CC kidney, brain or adrenal tumours, neuroblastoma, rhabdomyosarcoma,
XX CC leiomyosarcoma and/or lymphoma.
XX XX Sequence 4118 BP; 991 A; 1032 C; 1094 G; 1001 T; 0 other;

Query Match 90.7%; Score 669; DB 18; Length 4118;

Best Local Similarity 97.1%; Pred. No. 3.le-112;
Matches 681; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 38 CGGGATCCTCTAGAGTCGACCTGCAAGCTTGAAGCTTGTAGTATTCTAGTGTACCT 97
Db 942 cgtatgaccttgagcagtaggataaacacccacacagcttgattctctatagtcacct 1001
QY 98 AATAGCTTGGCGTAAATCATGGTTCATAGCTGTTCTCTGTTGTAATGTTATCCCTCACC 157
Db 1002 aatagcttggttaatactggttcttctggtgaaattgtta cccgctcac 1061
QY 158 AATTCACACACATACGAGCGGGAAGCTGTAAAGCTTGGGGTGCCTAATAGAT 217
Db 1062 aattccacacacatacagcgcggaagcgtgaaagcctggggtgctaatagat 1121
QY 218 GAGCTAACTCAGATTAATGCTGCTGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 277
Db 1122 gagctaaactcaattaatgctgctgctgctgctgctgctgctgctgctgctgctgct 1181
QY 278 GTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGAGAGCGGCTTTCGTTATGGGCG 337
Db 1182 gtgccagctgcattaatgaatcggccaaacgcgagggagagggcgtttgctattgggcg 1241
QY 338 CTCTTCGCTTCTCTGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 397
Db 1242 ctcttcgcttctctgctcactgactgctgctgctgctgctgctgctgctgctgctgctg 1301
QY 398 ATCAGCTCACTCAAAAGGGGGTAATACGGTTATTCACAGTAATCAGGGGATACCCAGGAAA 457
Db 1302 atcagctcactcaaaaggcgttaatacgggttatccacagaatcaggggataaacgagaaa 1361
QY 458 GAACATGTGAGCAAAAGGCGCAGCAAAAGCCAGGAAGCGTAAAGAGCCGCTGCTGCTGGC 517
Db 1362 gaacatgtgagcaaaaggcgcagcaaaaggccaggaacgcgttaaaaggccgctgctggc 1421
QY 518 GTTTTTCATAGGCTCCGCCCTCCCTGACGAGATCACAAAATCGCGCTCAAGTCAGAG 577
Db 1422 gtttttcataggtccgccctccctgacgagcatcaaaaaatcgcgtcaagtcagag 1481
QY 578 GTGCGCAACCCGACAGGACTATAAGATACAGCGCTTTCCTCCCTCGAAGCTCCCTCGT 637
Db 1482 gtgcgaaacccgcagagactataaagatacaggcgtttccctctggaagctccctcgt 1541
QY 638 GCGCTCTCTGTTCCGACCGCTGCGGTTACCGGATACCTGCTGCTGCTGCTGCTGCTGCTG 697
Db 1542 gcgctctctctgtccgacctgcgctaccgga tacctgcccgccttctctctctcggg 1601
QY 698 AAGCGTGGCGCTTTCATAGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 738
Db 1602 aagcgtggcgctttctctatagctcagcgttaggtatctca 1642

RESULT 11
AAT69189
ID AAT69189 standard; DNA; 4118 BP.
XX AC AAT69189;
XX AC AAT69189;
XX DT 26-FEB-1998 (first entry)
XX XX Construct pGEM-hTR(Ka) containing RNA component of human telomerase.
XX DE Human telomerase; quantification; tumour cell; pGEM-hTR(Ka);
XX KW detection; micrometastasis; diagnosis; lymphoblastoma; leukaemia;
XX KW teratocarcinoma; melanoma; carcinoma; cancer; tumour; neuroblastoma;
XX KW rhabdomyosarcoma; leiomyosarcoma; lymphoma; RNA component; ss.
XX XX Homo sapiens.
XX OS Synthetic.
XX XX WO9718322-A2.
XX PN 22-MAY-1997.
XX PD 22-MAY-1997.

PN WO200198485-A1.
XX
PD 27-DEC-2001.
XX
PF 20-JUN-2001; 2001WO-NZ00115.
XX
PR 20-JUN-2000; 2000US-0598401.
PR 28-NOV-2000; 2000US-0724624.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS IND LTD.
XX
XX Perera R, Rice S, Eagleton C, Lasham A;
PI
XX WPI; 2002-114583/15.
DR
XX
XX Novel polynucleotide promoter sequences from Pine and Eucalyptus useful
PT for modifying expression of endogenous and/or heterologous
PT polynucleotides in transgenic plants -
XX
XX Claim 1; Page 95; 121pp; English.
XX
XX The invention relates to isolated promoter sequences from pinus radiata
CC and Eucalyptus grandis, comprising a sequence chosen from leaf-, root-,
CC flower-, pollen-, bud-, meristem-specific promoters or temporally
CC regulated promoters such as xylogenesis-specific promoters. The promoter
CC polypeptides and their related polynucleotides are useful in the
CC production of genetic constructs, used for modifying gene expression in a
CC target organism, in particular a plant. The method is useful for
CC modifying expression of a polynucleotide that comprises an intron
CC sequence, through removal of the intron sequence. The method is useful
CC for modifying growth and development of plants, and cellular responses to
CC external stimulus, such as environmental factors and disease pathogens.
CC The sequences are useful in genome and physical mapping, in positional
CC cloning of genes, in various assays to determine biological activity, to
CC raise antibodies, to isolate corresponding interacting proteins and other
CC compounds, and to quantitatively determine levels of interacting proteins
CC or other compounds. Sequences ABK17016-ABK17125 represent pinus radiata
CC and Eucalyptus grandis polynucleotides and PCR primers used in the method
CC of the invention.
XX
XX Sequence 2571 BP; 659 A; 608 C; 635 G; 669 T; 0 other;

Search completed: August 1, 2002, 09:37:57
Job time: 6793 sec

Query Match 90.4%; Score 667; DB 24; Length 2571;
Best Local Similarity 100.0%; Pred. No. 7.Be-112;
Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 72 AGCTTGAGTATTCATAGTGTACCTAATAGCTTGGCGTAACTCATGTGTCATAGCTGTTT 131
DB 932 AGCTTGAGTATTCATAGTGTACCTAATAGCTTGGCGTAACTCATGTGTCATAGCTGTTT 873
QY 132 CCTGTGTGAATTTGTTATCCGCTCACAATTTCCACAAACATACGAGCCGGGAAGCATAAG 191
DB 872 CCTGTGTGAATTTGTTATCCGCTCACAATTTCCACAAACATACGAGCCGGGAAGCATAAG 813
QY 192 TGTAAAGCCTGGGCGCTAATAGTGTAGTGTACCTAATTTGCGTTCCTGCTGCTGCTGCTG 251
DB 812 TGTAAAGCCTGGGCGCTAATAGTGTAGTGTACCTAATTTGCGTTCCTGCTGCTGCTGCTG 753
QY 252 CCGGCTTTCCAGTCGGGAACCTGTGCTGCCAGCTGCATTAATGAATCGGCCAACGCGCG 311
DB 752 CCGGCTTTCCAGTCGGGAACCTGTGCTGCCAGCTGCATTAATGAATCGGCCAACGCGCG 693
QY 312 GGGAGAGCGGTTTGGCTATTGGGCGCTCTTCGCTTCCTGCTGCTGCTGCTGCTGCTG 371
DB 692 GGGAGAGCGGTTTGGCTATTGGGCGCTCTTCGCTTCCTGCTGCTGCTGCTGCTGCTG 633
QY 372 TCGGTCGTTTCGGCTGCGGCGAGCGGTATCAGCTCACAAGCGCGGTAAATACGGTTATCC 431
DB 632 TCGGTCGTTTCGGCTGCGGCGAGCGGTATCAGCTCACAAGCGCGGTAAATACGGTTATCC 573
QY 432 ACAGAATCAGGGGATAACGCGAGGAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGG 491

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OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 09:30:48 ; Search time 87.24 Seconds
(without alignments)
2077.918 Million cell updates/sec

Title: US-10-014-743-3
Perfect score: 738
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A-COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B-COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A-COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B-COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTCUS-COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	738	100.0	738	1	US-08-726-462B-3
2	738	100.0	738	2	US-09-046-203-3
3	738	100.0	738	3	US-09-272-104-3
4	738	100.0	738	4	US-09-272-097-3
5	672.4	91.1	4283	1	US-08-343-401A-3
6	672.4	91.1	4283	1	US-08-445-265A-1
7	672.4	91.1	4283	3	US-08-990-442-1
8	667.8	90.5	4539	1	US-08-119-512-1
9	667.8	90.5	4539	1	US-08-488-015B-1
10	667.8	90.5	4542	3	US-08-814-412-11
11	662.2	89.7	3485	4	US-08-939-366-10
12	660.4	89.5	10306	3	US-08-716-351A-4
13	660.4	89.5	10970	3	US-08-716-351A-5
14	659.4	89.3	9837	1	US-08-832-883-68
15	659.4	89.3	9837	2	US-08-832-883-68
16	650.8	88.2	4161	4	US-09-185-244-8
17	646.2	87.6	3918	2	US-08-495-500-2
18	641.6	86.9	8854	3	US-09-053-549-1
19	638.4	86.5	4824	2	US-08-485-139-5
20	638.4	86.5	4824	3	US-08-750-357-5
21	637.6	86.4	8710	1	US-08-480-882B-3
22	637.6	86.4	8710	1	US-08-480-210-3
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24	637.6	86.4	9019	1	US-08-480-210-4
25	637.6	86.3	3699	3	US-08-646-538-6
26	637.6	86.3	3699	4	US-09-503-222-6
27	637.6	86.3	3737	2	US-08-784-208-1

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2 US-08-792-824-1
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3 US-08-675-566-14
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2 US-08-472-809B-7
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3 US-08-776-511-3
3 US-08-675-566-16
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ALIGNMENTS

RESULT 1
US-08-726-462B-3
; Sequence 3, Application US/08726462B
; Patent No. 5800996
; GENERAL INFORMATION:
; APPLICANT: Perkin-Elmer Corporation, Applied Biosystems
; APPLICANT: Division
; TITLE OF INVENTION: ENERGY TRANSFER DYES WITH ENHANCED
; TITLE OF INVENTION: FLUORESCENCE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David J. Weltz
; ADDRESSEE: David J. Weltz, Wilson Sonsini Goodrich
; STREET: 650 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Microsoft Windows 3.1/DOS 5.0
; SOFTWARE: Wordperfect for Windows 6.0,
; SOFTWARE: ASCII (DOS) TEXT format
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,462B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/642,330
; FILING DATE: May 3, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/672,196
; FILING DATE: June 27, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: David J. Weltz
; REGISTRATION NUMBER: 38,362
; REFERENCE/DOCKET NUMBER: PELM4304
; TELEPHONE: (415) 493-9300
; TELEFAX: (415) 493-6811
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-726-462B-3


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; LOCATION: 981..1253
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(713..721, 981..1253)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 713..1049
; US-08-343-401A-3

Query Match          91.1%; Score 672.4; DB 1; Length 4283;
Best Local Similarity 99.9%; Pred. No. 5e-159;
Matches 673; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 65 GCATGCAAGCTTGAGTATTCATATAGTGTACCTAAATAGCTTGGCGTAAATCATGGTCATA 124
Db 1590 GCATGCAAGCTTGAGTATTCATATAGTGTACCTAAATAGCTTGGCGTAAATCATGGTCATA 1649

QY 125 GCTGTTTCTGTCGAAATGTTATTCGCTCACAATTCACACAAATAGAGCCGGAAG 184
Db 1650 GCTGTTTCTGTCGAAATGTTATTCGCTCACAATTCACACAAATAGAGCCGGAAG 1709

QY 185 CATAAAGTGAAGCTGGGCTGCTTAATGAGTGAAGTAACTCACAATTAATTCGTTGCG 244
Db 1710 CATAAAGTGAAGCTGGGCTGCTTAATGAGTGAAGTAACTCACAATTAATTCGTTGCG 1769

QY 245 CTCACGTGCGGCTTCCAGTTCGGGAACCTGCTGCCAGTGCATTAATGAATCGGCCA 304
Db 1770 CTCACGTGCGGCTTCCAGTTCGGGAACCTGCTGCCAGTGCATTAATGAATCGGCCA 1829

QY 305 ACGCGGGGAGAGCGGTTTGGTATTCGGCGCTCTTCCGCTTCCCTGCTCACTGACTC 364
Db 1830 ACGCGGGGAGAGCGGTTTGGTATTCGGCGCTCTTCCGCTTCCCTGCTCACTGACTC 1889

QY 365 GCTGCGCTCGGTCGTTGCGGCTGCGGAGCGGTATCAGCTCACTCAAAAGCGGTAAACG 424
Db 1890 GCTGCGCTCGGTCGTTGCGGCTGCGGAGCGGTATCAGCTCACTCAAAAGCGGTAAACG 1949

QY 425 GTTATCCACAGAATCAGGGGATAACGAGAAAGAAATCTGAGCAAAAGGCCAGCAAAA 484
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QY 485 GCGCAGAACCGTAAAAAGCGGTTGCTGGCGTTTTCATAGGCTCGGCCCTCG 544
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QY 665 TACCGGATACCTGTCGCGCTTTCCTTCCCTTCGGGAAGCGTGGCGCTTTCATAGCTCAG 724
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QY 725 CTGTAGGTATCTCA 738
Db 2250 CTGTAGGTATCTCA 2263

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RESULT 6
US-08-445-265A-1
; Sequence 1, Application US/08445265A
; Patent No. 5697901
; GENERAL INFORMATION:
; APPLICANT: Eriksson, Elof
; TITLE OF INVENTION: GENE DELIVERY BY MICRONEDLE INJECTION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady

```

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; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,265A
; FILING DATE:
; CLASSIFICATION: 604
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 110229, 91080
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4283 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Plasmid DNA"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(713..721, 981..1250)
; US-08-445-265A-1

Query Match          91.1%; Score 672.4; DB 1; Length 4283;
Best Local Similarity 99.9%; Pred. No. 5e-159;
Matches 673; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 65 GCATGCAAGCTTGAGTATTCATATAGTGTACCTAAATAGCTTGGCGTAAATCATGGTCATA 124
Db 1590 GCATGCAAGCTTGAGTATTCATATAGTGTACCTAAATAGCTTGGCGTAAATCATGGTCATA 1649

QY 125 GCTGTTTCTGTCGAAATGTTATTCGCTCACAATTCACACAAATAGAGCCGGAAG 184
Db 1650 GCTGTTTCTGTCGAAATGTTATTCGCTCACAATTCACACAAATAGAGCCGGAAG 1709

QY 185 CATAAAGTGAAGCTGGGCTGCTTAATGAGTGAAGTAACTCACAATTAATTCGTTGCG 244
Db 1710 CATAAAGTGAAGCTGGGCTGCTTAATGAGTGAAGTAACTCACAATTAATTCGTTGCG 1769

QY 245 CTCACGTGCGGCTTCCAGTTCGGGAACCTGCTGCCAGTGCATTAATGAATCGGCCA 304
Db 1770 CTCACGTGCGGCTTCCAGTTCGGGAACCTGCTGCCAGTGCATTAATGAATCGGCCA 1829

QY 305 ACGCGGGGAGAGCGGTTTGGTATTCGGCGCTCTTCCGCTTCCCTGCTCACTGACTC 364
Db 1830 ACGCGGGGAGAGCGGTTTGGTATTCGGCGCTCTTCCGCTTCCCTGCTCACTGACTC 1889

QY 365 GCTGCGCTCGGTCGTTGCGGCTGCGGAGCGGTATCAGCTCACTCAAAAGCGGTAAACG 424
Db 1890 GCTGCGCTCGGTCGTTGCGGCTGCGGAGCGGTATCAGCTCACTCAAAAGCGGTAAACG 1949

QY 425 GTTATCCACAGAATCAGGGGATAACGAGAAAGAAATCTGAGCAAAAGGCCAGCAAAA 484
Db 1950 GTTATCCACAGAATCAGGGGATAACGAGAAAGAAATCTGAGCAAAAGGCCAGCAAAA 2009

QY 485 GCGCAGAACCGTAAAAAGCGGTTGCTGGCGTTTTCATAGGCTCGGCCCTCG 544
Db 2010 GCGCAGAACCGTAAAAAGCGGTTGCTGGCGTTTTCATAGGCTCGGCCCTCG 2069

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Db 2130 ATACAGCGGTTTCCCGCTGGAAGCTCCCTCGCGCTCTCTGTTCCGACCCCTCGCGCT 2189
QY 665 TACCGGATACCTCGCGCTTCTCCCTTCGCGAAGCGTGGGCTTTCTCATAGCTCAG 724
Db 2190 TACCGGATACCTCGCGCTTCTCCCTTCGCGAAGCGTGGGCTTTCTCATAGCTCAG 2249
QY 725 CTGTAGGTATCTCA 738
Db 2250 CTGTAGGTATCTCA 2263

RESULT 7
US-08-990-442-1
; Sequence 1, Application US/08990442
; Patent No. 6090790
; GENERAL INFORMATION:
; APPLICANT: Eriksson, Elof
; TITLE OF INVENTION: GENE DELIVERY BY MICRONEEDLE INJECTION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pluckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/990,442
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berson, Bennett J
; REGISTRATION NUMBER: 37094
; REFERENCE/DOCKET NUMBER: 310558.90028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4283 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "plasmid DNA"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(713..721, 981..1250)
US-08-990-442-1

Query Match 91.1%; Score 672.4; DB 3; Length 4283;
Best Local Similarity 99.9%; Pred. No. 5e-159;
Matches 673; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 65 GCATCGAACCTTGAGTATCTATAGTGTACCTTAATAGCTTGGCGTAATCATGGTCATA 124
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QY 125 GCTGTTTCTGTGTAATTTGTTATCCGCTCACAAATCCACAAACATACGAGCCGGAAG 184
Db 1650 GCTGTTTCTGTGTAATTTGTTATCCGCTCACAAATCCACAAACATACGAGCCGGAAG 1709
QY 185 CATAAAGTGTAAGCCCTGGGTGGCTTAATGAGTGAGCTAACTACATTAATTCGTTGGC 244

Db 1710 CATAAAGTCGTAAGCCTGGGTGCGCTAATAGTGAGCTAACTACATTAATTCGTTGGC 1769
QY 245 CTCACATGCGCGCTTTCAGTCCGGAAACCTGCTGCGAGCTGCATTAATGAATCGGCCA 304
Db 1770 CTCACATGCGCGCTTTCAGTCCGGAAACCTGCTGCGAGCTGCATTAATGAATCGGCCA 1829
QY 305 ACSCGCGGGGAGAGCGGTTTTCGCTATTGGCGCTCTTCCGCTTCTCGCTCACTGACTC 364
Db 1830 ACSCGCGGGGAGAGCGGTTTTCGCTATTGGCGCTCTTCCGCTTCTCGCTCACTGACTC 1889
QY 365 GCTGCGCTGCTGCTGCTGCGGAGCGGTATCAGCTCAGTCMAAGCGGTAATACG 424
Db 1890 GCTGCGCTGCTGCTGCTGCGGAGCGGTATCAGCTCAGTCMAAGCGGTAATACG 1949
QY 425 GTTATCCACAGATCAGGGGATACGACGAGGAAAGAACATGTGAGCAAAAGGCCAGCAAA 484
Db 1950 GTTATCCACAGATCAGGGGATACGACGAGGAAAGAACATGTGAGCAAAAGGCCAGCAAA 2009
QY 485 GGCAGGAAACCGTAAAGAGCGCGTTCGTCGCGTTTTCATAGGCTCCGCCCCCTGA 544
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QY 545 CGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAG 604
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QY 605 ATACAGCGGTTTCCCGCTGGAAGCTCCCTCGCTGCTCTCTGTTCCGACCCCTGCGCT 664
Db 2130 ATACAGCGGTTTCCCGCTGGAAGCTCCCTCGCTGCTCTCTGTTCCGACCCCTGCGCT 2189
QY 665 TACCGGATACCTCGCGCTTCTCCCTTCGCGAAGCGTGGGCTTTCTCATAGCTCAG 724
Db 2190 TACCGGATACCTCGCGCTTCTCCCTTCGCGAAGCGTGGGCTTTCTCATAGCTCAG 2249
QY 725 CTGTAGGTATCTCA 738
Db 2250 CTGTAGGTATCTCA 2263

RESULT 8
US-08-119-512-1
; Sequence 1, Application US/08119512
; Patent No. 5498531
; GENERAL INFORMATION:
; APPLICANT: Jarrell, Kevin A.
; TITLE OF INVENTION: INTRON MEDIATED RECOMBINANT TECHNIQUES
; TITLE OF INVENTION: AND REAGENTS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/119,512
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: HUI-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:

[illegible]

APPLICATION NUMBER: US/08/939,366
FILING DATE: 29-SEP-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OHU-02749
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 3485 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-08-939-366-10

Query Match 89.7%; Score 662.2; DB 4; Length 3485;
Best Local Similarity 99.6%; Pred. No. 1.7e-156;
Matches 664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 72 AGCTTGAGTATCTATAGTCACCTAAATAGCTTGGCGTAATCATGGTCAATAGCTGTTT 131
Db 404 AGCTTGAGTATCTATAGTCACCTAAATAGCTTGGCGTAATCATGGTCAATAGCTGTTT 463

QY 132 COTGTGTGAATTTGTTATCCGCTCACAAATCCACAAACATAGAGCGGAAAGCAATAAG 191
Db 464 COTGTGTGAATTTGTTATCCGCTCACAAATCCACAAACATAGAGCGGAAAGCAATAAG 523

QY 192 TGTAAAGCTGGGTGCTAATGAGTACGTAACCTACATTAATTCGTTGGCTCACGTG 251
Db 524 TGTAAAGCTGGGTGCTAATGAGTACGTAACCTACATTAATTCGTTGGCTCACGTG 583

QY 252 CCCGCTTTCCAGTCGGGAAACCTGCTGCGCAGCTGCATTAATGAATCGGCCAACGCGG 311
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QY 312 GGGAGAGCGGTTTGGCTATTGGCGCTCTTCGCTTCCCTCGCTCACTACGCTCGCTGGC 371
Db 644 GGGAGAGCGGTTTGGCTATTGGCGCTCTTCGCTTCCCTCGCTCACTACGCTCGCTGGC 703

QY 372 TCGGTGCTTTCGGCTGCGCGAGCGGTATCAGCTCACTAAAGCGGTAATAGGTTATCC 431
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QY 552 CACAAAAATCAGCGCTCAAGTCAGAGTGGCGGAAACATGTAGCAAAAGGCCAGCAAGGCCAG 611
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QY 672 TACCTGTCGCGCTTTCCTCCCTTCGGGAAGCGTGGCGCTTTCATAGCTCACGCTGTAGG 731
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QY 732 TATCTCA 738
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RESULT 12

US-08-716-351A-4/c
Sequence 4, Application US/08716351A
Patent No. 6033905
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Gibbon Ape Leukemia Virus-Based
TITLE OF INVENTION: Retroviral Vectors
NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,351A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/03784
FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 15280-128-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10306 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..10258
OTHER INFORMATION: /standard_name= "p521 retroviral"
OTHER INFORMATION: vector"
US-08-716-351A-4

Query Match 89.5%; Score 660.4; DB 3; Length 10306;
Best Local Similarity 99.8%; Pred. No. 5.6e-156;
Matches 661; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 77 GAGTATTCTATAGTGCACCTAAATAGCTTGGCGTAATCATGGTCAATAGCTGTTTCTCTGT 136
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QY 137 GTGAAATTTGTTATCCGCTCACAAATCCACAAACATAGAGCGCGGAAAGCATAAAGTGTA 196
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QY 377 CGTTTCGGCTGCGCGAGCGGTATCAGCTCACTCAAAAGCGGTAATACGGTTATCCACAGA 436
Db 10006 CGTTTCGGCTGCGCGAGCGGTATCAGCTCACTCAAAAGCGGTAATACGGTTATCCACAGA 9947

QY 437 ATCAGGGGATAACGCAAGGAAAGCAATGTGAGCAAAAGGCCAGCAAAAGGCCAGGACCG 496

Db 9946 ATCAGGGGATAACGACGAGAAAGACATGTGAGCAAAAGGCCAGCAAAAGCCG 9887
QY 497 TAAAGGCGCGTGTGCTGCGCTTTTCATAGGCTCCGCGCCCTGAGGACATCAAA 556
Db 9886 TAAAGGCGCGTGTGCTGCGCTTTTCATAGGCTCCGCGCCCTGAGGACATCAAA 9827
QY 557 AAATCGAGCGCTCAAGTCAGAGTGGGGAACCCGACAGGACTATAAAGATACAGGCGTT 616
Db 9826 AAATCGAGCGCTCAAGTCAGAGTGGGGAACCCGACAGGACTATAAAGATACAGGCGTT 9767
QY 617 TCCCGCTGGAAGCTCCCTGCGCTGCTCTGTTCCGACCCCTTACCGGATACCT 676
Db 9766 TCCCGCTGGAAGCTCCCTGCGCTGCTCTGTTCCGACCCCTTACCGGATACCT 9707
QY 677 GTCCGCGCTTTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCT 736
Db 9706 GTCCGCGCTTTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCT 9647
QY 737 CA 738
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RESULT 13

US-08-716-351A-5/c
; Sequence 5, Application US/08716351A
; Patent No. 6033905
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Gibbon Ape Leukemia Virus-Based
; TITLE OF INVENTION: Retroviral Vectors
; NUMBER OF SEQUENCES: 5
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/716,351A
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/03784
; FILING DATE: 06-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian,, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 15280-128-1PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..10970
; OTHER INFORMATION: /standard_name= "p537 retroviral"
; OTHER INFORMATION: vector"
US-08-716-351A-5

Query Match 89.5%; Score 660.4; DB 3; Length 10970;
Best Local Similarity 99.8%; Pred. No. 5.7e-156;
Matches 661; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 77 GAGTATCTATAGTGTACCTCAATAGCTTGGCGTAAATCATGCTACAGCTTTTCCTGT 136
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Db 10970 GAGTATCTATAGTGTACCTCAATAGCTTGGCGTAAATCATGCTACAGCTTTTCCTGT 10911
QY 137 GTCAAAATTCCTTATCCGCTCACAAATTTCCACAAACATACGAGCCGGAAGCATAAAGTGTAA 196
Db 10910 GTGAAATTCCTTATCCGCTCACAAATTTCCACAAACATACGAGCCGGAAGCATAAAGTGTAA 10851
QY 197 AGCGTGGGTGCTTAAATGAGTAGCTAACTACACATTAATTCGCTTGGCTCTACTGCCCCG 256
Db 10850 AGCGTGGGTGCTTAAATGAGTAGCTAACTACACATTAATTCGCTTGGCTCTACTGCCCCG 10791
QY 257 TTTCCAGTCGGGAAACCTGCTGCGCCAGCTGCATTAATGAATCGGCCCAAGCCGCGGGAG 316
Db 10790 TTTCCAGTCGGGAAACCTGCTGCGCCAGCTGCATTAATGAATCGGCCCAAGCCGCGGGAG 10731
QY 317 AGCGGTGTTGCGTATTTGGGCGCTCTTCGCTTCCTGCTCACTGACTCGCTGCGCTCGGT 376
Db 10730 AGCGGTGTTGCGTATTTGGGCGCTCTTCGCTTCCTGCTCACTGACTCGCTGCGCTCGGT 10671
QY 377 CGTTCGGCTGCGCGGAGGATATCAGCTCACTCAAAAGCGGTAAATACGCTTATCCACAGA 436
Db 10670 CGTTCGGCTGCGCGGAGGATATCAGCTCACTCAAAAGCGGTAAATACGCTTATCCACAGA 10611
QY 437 ATCAGGGGATAACGACGAGGAAAGACATGTGAGCAAAAGGCGCAGAAAAGGCCAGGAACCG 496
Db 10610 ATCAGGGGATAACGACGAGGAAAGACATGTGAGCAAAAGGCGCAGAAAAGGCCAGGAACCG 10551
QY 497 TAAAAAGCGCGCTTGTGGCGTTTTTCCATAGGCTCGCGCCCTCAGCAGCATCAAA 556
Db 10550 TAAAAAGCGCGCTTGTGGCGTTTTTCCATAGGCTCGCGCCCTCAGCAGCATCAAA 10491
QY 557 AAATCAGCTCAAGTCAGAGGTGCGGAAACCCGACAGGACTATAAAGATACACGCGTT 616
Db 10490 AAATCAGCTCAAGTCAGAGGTGCGGAAACCCGACAGGACTATAAAGATACACGCGTT 10431
QY 617 TCCCGCTGGAAGCTCCCTGCTGCGCTCTCTGTTCCGACCTGCGCTTACCGGATACCT 676
Db 10430 TCCCGCTGGAAGCTCCCTGCTGCGCTCTCTGTTCCGACCTGCGCTTACCGGATACCT 10371
QY 677 GTCCGCGTTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTACAGCTGTAGGTATCT 736
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QY 737 CA 738
Db 10310 CA 10309

RESULT 14

US-08-832-883-68/c
; Sequence 68, Application US/08832883
; Patent No. 5807681
; GENERAL INFORMATION:
; APPLICANT: Giordano, Antonio
; APPLICANT: Baldi, Alphonso
; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS
; TITLE OF INVENTION: OF CANCER
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
; STREET: Suite 1800 Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/832,883
; FILING DATE:
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A
REGISTRATION NUMBER: 30,480
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 9837 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-832-883-68

Query Match 89.3%; Score 659.4; DB 1; Length 9837;
Best Local Similarity 95.6%; Pred. No. 9.9e-156;
Matches 689; Conservative 0; Mismatches 31; Indels 1; Gaps 1;
Qy 18 GGAATTCAGCTCGGTACCGGGGATCCTCTAGAGTCGACCTGCGAGCATGCAAGCTTG 77
Db 7217 GCACACTGCGCGCGCTTACTAGTCGATCCGAGCTCGGTACCAAGCTTGTATGTCATAGCTTG 7158
Qy 78 AGTATTCATAGTGCACCTAAATAGCTTGGCGTAATCATGCTCATAGCTGTTTCCTGTG 137
Db 7157 AGTATTCATAGTGCACCTAAATAGCTTGGCGTAATCATGCTCATAGCTGTTTCCTGTG 7098
Qy 138 TGAATTTGTTATCGGTCACAATTCCACACACATACGAGCGCGGAAGCAATAAGTGATAA 197
Db 7097 TGAATTTGTTATCGGTCACAATTCCACACACATACGAGCGCGGAAGCAATAAGTGATAA 7038
Qy 198 GCCTGGGTGCCTAAATGAGTGAGTCACTCAATTAATTCGCTTCCGCTCACTGCCCGCT 257
Db 7037 GCCT-GGGTGCCTAAATGAGTGAGTCACTCAATTAATTCGCTTCCGCTCACTGCCCGCT 6979
Qy 258 TTCCAGTCGGGAACCTGTCGTCGCCAGCTGCAATTAATGAGTCACTGCCCGCTCACTGCCCGCT 317
Db 6978 TTCCAGTCGGGAACCTGTCGTCGCCAGCTGCAATTAATGAGTCACTGCCCGCTCACTGCCCGCT 6919
Qy 318 GCGGTTTGGGTATTTGGGCGCTCTTCCGCTTCCGCTCACTGCCCGCTCACTGCCCGCT 377
Db 6918 GCGGTTTGGGTATTTGGGCGCTCTTCCGCTTCCGCTCACTGCCCGCTCACTGCCCGCT 6859
Qy 378 GTTCGCTGCGGCGAGCGGTATCAGCTCACTCAAGCGGTAAATAGCTTATCCACAGAA 437
Db 6498 A 6498

RESULT 15
US-08-832-877-68/c
Sequence 68, Application US/08832877
Patent No. 5840506
GENERAL INFORMATION:
APPLICANT: Giordano, Antonio
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS OF
TITLE OF INVENTION: CANCER
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEIDEL, CONDA, LAVORGNA & MONACO, P.C.
STREET: Suite 1800 Two Penn Center Plaza
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,877
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-13 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 9837 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-832-877-68

Query Match 89.3%; Score 659.4; DB 2; Length 9837;
Best Local Similarity 95.6%; Pred. No. 9.9e-156;
Matches 689; Conservative 0; Mismatches 31; Indels 1; Gaps 1;
Qy 18 GCGAATTCGAGCTCGGTACCGGGGATCCTCTAGAGTCGACCTGCGAGCATGCAAGCTTG 77
Db 7217 GCACACTGCGCGCGCTTACTAGTCGATCCGAGCTCGGTACCAAGCTTGTATGTCATAGCTTG 7158
Qy 78 AGTATTCATAGTGCACCTAAATAGCTTGGCGTAATCATGCTCATAGCTGTTTCCTGTG 137
Db 7157 AGTATTCATAGTGCACCTAAATAGCTTGGCGTAATCATGCTCATAGCTGTTTCCTGTG 7098
Qy 138 TGAATTTGTTATCGGTCACAATTCCACACACATACGAGCGCGGAAGCAATAAGTGATAA 197
Db 7097 TGAATTTGTTATCGGTCACAATTCCACACACATACGAGCGCGGAAGCAATAAGTGATAA 7038
Qy 198 GCCTGGGTGCCTAAATGAGTGAGTCACTCAATTAATTCGCTTCCGCTCACTGCCCGCT 257
Db 7037 GCCT-GGGTGCCTAAATGAGTGAGTCACTCAATTAATTCGCTTCCGCTCACTGCCCGCT 6979
Qy 258 TTCCAGTCGGGAACCTGTCGTCGCCAGCTGCAATTAATGAGTCACTGCCCGCTCACTGCCCGCT 317
Db 6978 TTCCAGTCGGGAACCTGTCGTCGCCAGCTGCAATTAATGAGTCACTGCCCGCTCACTGCCCGCT 6919
Qy 318 GCGGTTTGGGTATTTGGGCGCTCTTCCGCTTCCGCTCACTGCCCGCTCACTGCCCGCT 377
Db 6918 GCGGTTTGGGTATTTGGGCGCTCTTCCGCTTCCGCTCACTGCCCGCTCACTGCCCGCT 6859
Qy 378 GTTCGCTGCGGCGAGCGGTATCAGCTCACTCAAGCGGTAAATAGCTTATCCACAGAA 437
Db 6498 A 6498

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Db 6858 GTTCGGCTCGCGAGCGGTATCAGCTCACTCAAGGGGTAAATACGGTTATCCACAGAA 6799
QY 438 TCAGGGGATACGCGAGGAAGAACATGTGAGCAAAAGCCAGCAAAAGGCCAGGAACCGT 497
Db 6798 TCAGGGGATACGCGAGGAAGAACATGTGAGCAAAAGCCAGCAAAAGGCCAGGAACCGT 6739
QY 498 AAAAAGCGCGCGTTGCTGCGCTTTTCCATAGGCTCCGCCGCCCTGACGAGCATCACAAA 557
Db 6738 AAAAAGCGCGCGTTGCTGCGCTTTTCCATAGGCTCCGCCGCCCTGACGAGCATCACAAA 6679
QY 558 AATCGACGCTCAAGTCAGAGTGGCGAAACCCGACAGCACTATAAGATACCGGCGTTT 617
Db 6678 AATCGACGCTCAAGTCAGAGTGGCGAAACCCGACAGCACTATAAGATACCGGCGTTT 6619
QY 618 CCCCCGTGAAGCTCCCTCGCTCTCTCTGTTCCGACCCCTGCCGCTTACCGGATACCTG 677
Db 6618 CCCCCGTGAAGCTCCCTCGCTCTCTCTGTTCCGACCCCTGCCGCTTACCGGATACCTG 6559
QY 678 TCGGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGATGATATCTC 737
Db 6558 TCGGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGATGATATCTC 6499
QY 738 A 738
Db 6498 A 6498

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Search completed: August 1, 2002, 09:31:23
 Job time: 6644 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 08:39:47 ; Search time 2971.21 seconds
(without alignments)
3352.423 Million cell updates/sec

Title: US-10-014-743-3

Perfect score: 738

Sequence: 1 ATACGACTCACATATAGGCG.....CTCAGCGCTGATGATCTCA 738

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	713.4	96.7	838	12	AZ679307 ENTGL84TF
3	688.8	93.3	692	12	AQ040352 CIT-HSP-2
4	678.8	92.0	906	12	AZ549573 ENTFO03TF
5	665	90.1	666	12	AQ079096 CIT-HSP-2
6	661	89.6	891	12	AZ540838 ENTET16TF
7	653.8	88.6	683	10	BE662810 EST00554
8	652	88.3	652	12	AQ108633 CIT-HSP-2
9	651.4	88.3	653	12	AQ077504 CIT-HSP-2
10	651.2	88.2	667	10	BE430218 SUN000.D1
11	647.2	87.7	661	12	AQ057603 CIT-HSP-2
12	637.6	86.4	735	9	AV731085 AV731085
13	637	86.3	1039	9	AU081040 AU081040
14	637	86.3	1089	9	AU081124 AU081124
15	637	86.3	1163	9	AU081044 AU081044
16	636.6	86.3	1583	12	BH173601 BH173601
17	633.8	85.9	1067	9	AU081137 AU081137

18	631.4	85.6	633	12	AQ040787
19	627.6	85.0	642	12	AQ113213
20	625	84.7	996	9	AU081097
21	624.4	84.6	634	12	AQ038010
22	621.4	84.2	640	12	AQ074298
23	621.2	84.2	626	12	AQ111342
24	618.6	83.8	637	12	AQ077360
25	618.4	83.8	788	9	AJ281697
26	618	83.7	818	10	BI180988
27	615	83.3	823	12	AQ081172
28	609	82.5	1101	12	CNS00G5U
29	608.4	82.4	725	10	BI937939
30	606.2	82.1	735	10	BI938757
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33	605.6	82.1	711	10	BI938755
34	604.4	81.9	686	10	BI941052
35	603.8	81.8	708	10	BI675834
36	603.4	81.8	605	12	AQ077353
37	599.8	81.3	689	10	BI937753
38	599.2	81.2	612	12	AQ080586
39	598.6	81.1	725	10	BI937927
40	597.6	81.0	704	10	BI938042
41	596.8	80.9	725	10	BI938759
42	594	80.5	704	10	BI937386
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45	590	79.9	663	10	BI940725

ALIGNMENTS

RESULT 1

AZ687169
LOCUS ENTMP05TF Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, DNA sequence.
DEFINITION
ACCESSION AZ687169.1 GI:11824315
VERSION
KEYWORDS Entamoeba histolytica.
SOURCE Entamoeba histolytica
ORGANISM Eukaryota; Entamoebidae; Entamoeba.
REFERENCE 1 (bases 1 to 847)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
Unpublished (2000)
CONTACT: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjoftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library
Seq primer: M13-Forward
Class: shotgun
High quality sequence start: 63
High quality sequence stop: 291.
Location/Qualifiers
1. .847
/organism="Entamoeba histolytica"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a

method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Borell, Oxford University Press, 1999)."

BASE COUNT 182 a 245 c 221 g 199 t

Query Match 98.38; Score 725.4; DB 12; Length 847;
Best Local Similarity 99.7%; Pred. No. 3.6e-199;
Matches 737; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Db 7 ATACGACTACTATAGTGCGCAATTCGAGTCGCTACCCGGGATCCTCTAGAGTCGACC 66
|||||
QY 60 TCGAGCATGCAAGCTTGAGTATCTATAGTGCACCTAAATAGTGGGTGAATCATGG 119
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Db 67 TCGAGCATGCAAGCTTGAGTATCTATAGTGCACCTAAATAGTGGGTGAATCATGG 126
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QY 120 TCATAGCTGTTTCTGCTGTAATGTTATCCGCTCAATTCACACACATACGAGCC 179
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Db 127 TCATAGCTGTTTCTGCTGTAATGTTATCCGCTCAATTCACACACATACGAGCC 186
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QY 180 GGAAGCATAAAGTGTAAAGCTGGGTGCTTAATGATGAGTGAAGTCAATTAATGGC 239
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Db 187 GGAAGCATAAAGTGTAAAGCTGGGTGCTTAATGATGAGTGAAGTCAATTAATGGC 246
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QY 240 TTGCGCTCACTGCGCGTTCAGTTCGGAACCTGTCGTCGAGCTGCAATTAATGAATC 299
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Db 247 TTGCGCTCACTGCGCGTTCAGTTCGGAACCTGTCGTCGAGCTGCAATTAATGAATC 306
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QY 300 GCCAACCGCGGGAGAGCGGTTTGGTATGGGGCTCTTCCGCTTCCCTGCTCACT 359
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Db 307 GCCAACCGCGGGAGAGCGGTTTGGTATGGGGCTCTTCCGCTTCCCTGCTCACT 366
|||||
QY 360 GACTCGCTGCGCTCGGCTCGGCGAGCGGTATCAGCTCACTCAAGGCGGTA 419
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Db 367 GACTCGCTGCGCTCGGCTCGGCGAGCGGTATCAGCTCACTCAAGGCGGTA 426
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QY 420 ATACGTTATCCACAGATCAGGAGTAAGCCAGGAAGACATGTGACCAAGGCCAG 479
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QY 480 CAAAGGCCAGAACCGTAAAGGCCGCGTTGCTGCGCTTTTCCATAGGCTCCGCCCC 539
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Db 487 CAAAGGCCAGAACCGTAAAGGCCGCGTTGCTGCGCTTTTCCATAGGCTCCGCCCC 546
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QY 540 CCTGACGAGCATCAAAAATCGAGCTCAAGTCAGAGTGGCGAACCAGCAGGACTA 599
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Db 547 CTTGACGAGCATCAAAAATCGAGCTCAAGTCAGAGTGGCGAACCAGCAGGACTA 606
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Db 607 TAAAGTACAGGCGTTTCCCTTGGAGCTCCCTGTCGCGCTCTCTGTCGACCCCTG 666
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QY 660 CCGCTTACCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAGCGTGGCTTCTCATAGC 719
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Db 667 CCGCTTACCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAGCGTGGCTTCTCATAGC 726
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QY 720 TCACGCTGTAGTATCTCA 738
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Db 727 TCACGCTGTAGTATCTCA 745
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RESULT 2
A2679307
LOCUS ENT1G84TF Entamoeba histolytica 838 bp DNA linear GSS 14-DEC-2000
DEFINITION ENT1G84TF Entamoeba histolytica Sheared DNA Entamoeba histolytica

genomic, DNA sequence.
A2679307
A2679307.1 GI:11816453
GSS.
Entamoeba histolytica.
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 838)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
DNA library
Seq primer: M13-Forward
Class: shotgun
High quality sequence start: 52
High quality sequence stop: 297.
FEATURES
source
1..838
Location/Qualifiers
/organism="Entamoeba histolytica"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site: 1; Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark, A.
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Borell, Oxford University Press, 1999)."

BASE COUNT 186 a 235 c 221 g 196 t

Query Match 96.7%; Score 713.4; DB 12; Length 838;
Best Local Similarity 99.2%; Pred. No. 1.1e-195;
Matches 717; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 16 GGGGGAATTCGAGCTCGGTACCGGGGATCCTCTAGAGTCGACCTGCGAGGATCAAGCT 75
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Db 29 GGTGGAATTCGAGCTCGGTACCGGGGATCCTCTAGAGTCTTCTGCGAGGATCAAGCT 88
|||||
QY 76 TGAGTATTCATAGTGTCACTCAATATAGCTTGGCGCTAATCATGTGTCTAGTGTCTG 135
|||||
Db 89 TGAGTATTCATAGTGTCACTCAATATAGCTTGGCGCTAATCATGTGTCTAGTGTCTG 148
|||||
QY 136 TGTGAATTCGTTATCCGCTCACAATTCACACACATACGAGCCGGAAGCAATAAGTGA 195
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Db 149 TGTGAATTCGTTATCCGCTCACAATTCACACACATACGAGCCGGAAGCAATAAGTGA 208
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QY 196 AAGCCTGGGTGCCTAATGAGTGAAGTAACTCACAATTAATTCGCTTCACTGCGCCG 255
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Db 209 AAGCCTGGGTGCCTAATGAGTGAAGTAACTCACAATTAATTCGCTTCACTGCGCCG 268
|||||
QY 256 CTTTCCAGTCGGGAACCTGTCGCCAGCTCATTAAATGAATGATGATGATGATGATGATG 315
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Db 269 CTTTCCAGTCGGGAACCTGTCGCCAGCTCATTAAATGAATGATGATGATGATGATGATG 328
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QY 316 GAGCGGTTTGGGTATTTGGGGCGCTCTTCCGCTTCCTCGCTCACTGCTGCGCTCGG 375
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Db 329 GAGCGGTTTGGATTGGGCGCTCTCCGCTTCTCGCTCACTGACTCGCTGCGCTCG 388
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Db 389 TCGTTTCGGCTCGCGGAGCGGTATCAGCTCACTCAAGGCGGTAATACGTTATCCACAG 448
QY 436 AATCAGGGATTAACGACGAAGAATGTCAGCAAAAGCCAGCAAAAGCCAGCAAAACC 495
Db 449 AATCAGGGATTAACGACGAAGAATGTCAGCAAAAGCCAGCAAAAGCCAGCAAAACC 508
QY 496 GTAAAAAGCGCGCTTGTGCGCTTTTCCATAGGCTCCGCCCTCCGCTGACGAGCATCACA 555
Db 509 GTAAAAAGCGCGCTTGTGCGCTTTTCCATAGGCTCCGCCCTCCGCTGACGAGCATCACA 568
QY 556 AAAATCGAGCTCAAGTCAGAGTGGCGAAACCCGACAGCACTATAAGATACCAGGCT 615
Db 569 AAAATCGAGCTCAAGTCAGAGTGGCGAAACCCGACAGCACTATAAGATACCAGGCT 628
QY 616 TTCCCGCTGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCTTCCGCTTACCGGATAC 675
Db 629 TTCCCGCTGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCTTCCGCTTACCGGATAC 688
QY 676 TGTCCGCTTTCCTCCGTCGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATC 735
Db 689 TGTCCGCTTTCCTCCGTCGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATC 748
QY 736 TCA 738
Db 749 TCA 751
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RESULT 3

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LOCUS A040352 692 bp DNA linear GSS 11-JUL-1998
DEFINITION CIT-HSP-2327K21.TF CIT-HSP Homo sapiens genomic clone 2327K21, DNA
sequence.
ACCESSION A040352
VERSION A040352.1 GI:3306184
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 692)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building. (1998)
Unpublished (1998)
Other_GSSs: CIT-HSP-2327K21.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
FEATURES
source Location/Qualifiers
1..692
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2327K21"
/clone_lib="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelOBAC11; Site_1: HindIII; Site_2:
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BASE COUNT 158 a 193 c 186 g 155 t
ORIGIN
Query Match 93.3%; Score 688.8; DB 12; Length 692;
Best Local Similarity 99.7%; Pred. No. 1.3e-188;
Matches 690; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 16 GGCGGAATTCGAGCTCGGTACCGGGATCCTCTAGAGTCGACCTCGACGAGCATCGAAGCT 75
Db 1 GGCGGAATTCGAGCTCGGTACCGGGATCCTCTAGAGTCGACCTCGACGAGCATCGAAGCT 60
QY 76 TGAGTATTTCTATAGTGTACCTAAATAGCTTGGCGTAATCATGTGTCATAGCTGTTTCCTG 135
Db 61 TGAGTATTTCTATAGTGTACCTAAATAGCTTGGCGTAATCATGTGTCATAGCTGTTTCCTG 120
QY 136 TGTGAATTTCTATCGCTCACAAATTCACACAAATTCACAGCCGGAAGCATAAAGTGT 195
Db 121 TGTGAATTTCTATCGCTCACAAATTCACACAAATTCACAGCCGGAAGCATAAAGTGT 180
QY 196 AAGCTCGGGTGCCTAATGAGTGAGCTAACTCACATTAATTCGCTTGCCTCACTGCGCG 255
Db 181 AAGCTCGGGTGCCTAATGAGTGAGCTAACTCACATTAATTCGCTTGCCTCACTGCGCG 240
QY 256 CTTTCCAGTCGGGAACCTGTGTCGCCAGCTGCATTAATGAATCGGCCAAGCGGGGGA 315
Db 241 CTTTCCAGTCGGGAACCTGTGTCGCCAGCTGCATTAATGAATCGGCCAAGCGGGGGA 300
QY 316 GAGCGGTTTTCGCTATTGGCGCTCTTCGCTTCTCGCTCACTCACTGCTGCGCTCGG 375
Db 301 GAGCGGTTTTCGCTATTGGCGCTCTTCGCTTCTCGCTCACTCACTGCTGCGCTCGG 360
QY 376 TCGTTTCGGCTCGCGGAGCGGTATCAGCTCACTCAAAAGCGGTAAATACGGTTATCCACAG 435
Db 361 TCGTTTCGGCTCGCGGAGCGGTATCAGCTCACTCAAAAGCGGTAAATACGGTTATCCACAG 420
QY 436 AATCAGGGGATTAACGAGGAAGAACATGTGAGCAAAAGCCAGCAAAAGCCAGGAACC 495
Db 421 AATCAGGGGATTAACGAGGAAGAACATGTGAGCAAAAGCCAGCAAAAGCCAGGAACC 480
QY 496 GTAAAAAGCGCGCTTGTGCGCTTTTCCATAGGCTCGCGCCCTCGACGAGCATCACA 555
Db 481 GTAAAAAGCGCGCTTGTGCGCTTTTCCATAGGCTCGCGCCCTCGACGAGCATCACA 540
QY 556 AAAATCGACCTCAAGTCAGAGTGGCGAAACCCGACAGAGCTATAAAGATACCAAGGCT 615
Db 541 AAAATCGACCTCAAGTCAGAGTGGCGAAACCCGACAGAGCTATAAAGATACCAAGGCT 600
QY 616 TTCCCGCTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTGCGGTTACCGGATACC 675
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QY 676 TGTCCGCTTTCCTCCCTTCGCGGAAGCGTGGCG 707
Db 661 TGTCCGCTTTCCTCCCTTCGCGGAAGCGTGGCG 692
RESULT 4
AZ549573
LOCUS ENTUF03TF Entamoeba histolytica Sheared DNA linear GSS 14-NOV-2000
DEFINITION genomic, DNA sequence.
ACCESSION AZ549573
VERSION AZ549573.1 GI:11174314
KEYWORDS GSS.
ORGANISM Entamoeba histolytica.
SOURCE Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
REFERENCE 1 (bases 1 to 906)
AUTHORS Loftus,B., Van Aken,S. and Fraser,C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
```


JOURNAL
COMMENT

Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:INSS sheared
DNA library
Seq primer: M13-Forward
Class: Shotgun
High quality sequence start: 141
High quality sequence stop: 293.
Location/Qualifiers
1. .906
/organism="Entamoeba histolytica"
/strain="HMI:INSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
Note=Vector: PHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."

FEATURES

source

RESULT 5

A0079096

LOCUS

DEFINITION

A0079096

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

Query Match

Best Local Similarity

Matches 701; Conservative

0; Mismatches 37; Indels 0; Gaps 0;

YQ 1 ATACGACTCACTATAGGCGAATTCGAGCTCGGTACCGGGATCTCTAGAGTCGACCT 60

DB 10 ATACGACTGACTATAGGCGAATTCGAGCTCAGGACCGGGATCTCTAGAGTCGACCT 69

YQ 61 GCAGCATGCAAGCTTGAGTATCTATAGTGTCACTAAATAGCTTGGCGTAAATCATGTT 120

DB 70 GCATCATGCAAGCTTGAGTATCTATAGTGTCACTAAATAGCTTGGCGTAAATCATGTT 129

YQ 121 CATAGCTGTTCTCTGTGTAATTTATCGCTCAACAATTCACACACATACGAGCG 180

DB 130 CATAGCTGTTCTCTGTGTAATTTATCGCTCAACAATTCACACACATACGAGCG 189

YQ 181 GAAGCATAAAGTGTAAAGCTTGGGTGCTTAATAGTGTAGCTTAACATCAATTAATGCTT 240

DB 190 GAAGCATAAAGTGTAAAGCTTGGGTGCTTAATAGTGTAGCTTAACATCAATTAATGCTT 249

YQ 241 TCGCTGCTACTGCGGCTTTCAGTCGGGAAACCTGTCGTCGACGCTGCAATTAATGAATCG 300

DB 250 GCGCTCACTGCCGCTTTCAGTCGGGAAACCTGTCGTCGACGCTGCAATTAATGAATCG 309

YQ 301 GCCACGCGCGGGAGAGCGGTTGGGTATTTGGGCGCTTCCCGCTTCCCTCGCTCACTG 360

DB 310 GCCACGCGCGGGAGAGCGGTTGGGTATTTGGGCGCTTCCCGCTTCCCTCGCTCACTG 369

YQ 361 ACTCGCTGCGTCTGCTGCTGCGGCGAGCGGTATCAGCTCACTCACTCAAAAGCGGTA 420

DB 370 ACTCGCTGCGTCTGCTGCTGCGGCGAGCGGTATCAGCTCACTCACTCAAAAGCGGTA 429

YQ 421 TACGCTTATCACAGATCAGGGAATACCGAGGAAAGACATGTGAGCAAAAGGCCAGC 480

DB 430 TACGCTTATCACAGATCAGGGAATACCGAGGAAAGACATGTGAGCAAAAGGCCAGC 489

YQ 481 AAAAGGCCAGAACCGTAAAAAGCGCGTGTGCTGGCGTTTTCATATAGGCTCGGCCCC 540
DB 490 ATATCCCATGAACCGTAAAAAGCGCGTGTGCTGGCGTATTTCCATATAGGCTCGGCCCC 549
YQ 541 CTGACGAGCATCAAAAAATCAGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTAT 600
DB 550 CTGACGAGCATCAAAAAATCAGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTTA 609
YQ 601 AAGATACACAGGCTTCCCTCCCTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTGC 660
DB 610 TAGATACCATCGGTTTCCCTCCCTGGAAGCTCAAGCGCTCTCTGTTAGGACCTGC 669
YQ 661 CGTTTACCGGATACCTGTCGCGCTTCTCCCTTCGGAAGCGTGGCGTTCCTCATAGCT 720
DB 670 CGTTTACCGGATACCTGTCGCGCTTCTCCCTTCGGAAGCGTGGCGTTCCTCATAGCT 729
YQ 721 CACGCTGTAGTATCTCA 738
DB 730 CACGCTGTAGTATCTCA 747

RESULT 5

A0079096

LOCUS

DEFINITION

A0079096

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

YQ 1 ATACGACTCACTATAGGCGAATTCGAGCTCGGTACCGGGATCTCTAGAGTCGACCT 60

DB 10 ATACGACTGACTATAGGCGAATTCGAGCTCAGGACCGGGATCTCTAGAGTCGACCT 69

YQ 61 GCAGCATGCAAGCTTGAGTATCTATAGTGTCACTAAATAGCTTGGCGTAAATCATGTT 120

DB 70 GCATCATGCAAGCTTGAGTATCTATAGTGTCACTAAATAGCTTGGCGTAAATCATGTT 129

YQ 121 CATAGCTGTTCTCTGTGTAATTTATCGCTCAACAATTCACACACATACGAGCG 180

DB 130 CATAGCTGTTCTCTGTGTAATTTATCGCTCAACAATTCACACACATACGAGCG 189

YQ 181 GAAGCATAAAGTGTAAAGCTTGGGTGCTTAATAGTGTAGCTTAACATCAATTAATGCTT 240

DB 190 GAAGCATAAAGTGTAAAGCTTGGGTGCTTAATAGTGTAGCTTAACATCAATTAATGCTT 249

YQ 241 TCGCTGCTACTGCGGCTTTCAGTCGGGAAACCTGTCGTCGACGCTGCAATTAATGAATCG 300

DB 250 GCGCTCACTGCCGCTTTCAGTCGGGAAACCTGTCGTCGACGCTGCAATTAATGAATCG 309

YQ 301 GCCACGCGCGGGAGAGCGGTTGGGTATTTGGGCGCTTCCCGCTTCCCTCGCTCACTG 360

DB 310 GCCACGCGCGGGAGAGCGGTTGGGTATTTGGGCGCTTCCCGCTTCCCTCGCTCACTG 369

YQ 361 ACTCGCTGCGTCTGCTGCTGCGGCGAGCGGTATCAGCTCACTCACTCAAAAGCGGTA 420

DB 370 ACTCGCTGCGTCTGCTGCTGCGGCGAGCGGTATCAGCTCACTCACTCAAAAGCGGTA 429

YQ 421 TACGCTTATCACAGATCAGGGAATACCGAGGAAAGACATGTGAGCAAAAGGCCAGC 480

DB 430 TACGCTTATCACAGATCAGGGAATACCGAGGAAAGACATGTGAGCAAAAGGCCAGC 489

FEATURES

source

1. .866

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="2356E24"

/sex="Male"

/cell_type="Sperm"

/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:

HindIII"

BASE COUNT 156 a 186 c 174 g 149 t 1 others

ORIGIN

Query Match 90.1%; Score 665; DB 12; Length 666;

Best Local Similarity 99.8%; Pred. No. 1e-181;

Matches 665; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

YQ 21 AATTCGAGCTCGGTACCGGGGATCTCTAGAGTCGACCTGACGATGCAAGCTTGAGT 80

DB 1 AATTCGAGCTCGGTACCGGGGATCTCTAGAGTCGACCTGACGATGCAAGCTTGAGT 60

QY 81 ATTCTATAGTGTACCTAAATAGCTTGGCGTAATCATGTCATAGCTGTTTCTGTTGTA 140
 Db 61 ATCTATAGTGTACCTAAATAGCTTGGCGTAATCATGTCATAGCTGTTTCTGTTGTA 120
 QY 141 AATTGTTATCCGCTCACAAATCCACAAATACAGCGCGGAAGCAATAAGTGTAAAGCC 200
 Db 121 AATTGTTATCCGCTCACAAATCCACAAATACAGCGCGGAAGCAATAAGTGTAAAGCC 180
 QY 201 TGGGGTGCCTAATAGTGTAGTCACTACATTAATTCGGTTGGCGTCACTGCCCGCTTTC 260
 Db 181 TGGGGTGCCTAATAGTGTAGTCACTACATTAATTCGGTTGGCGTCACTGCCCGCTTTC 240
 QY 261 CAGTCGGGAACCTGCTGCGCAGTGCATTAATGAATCGGCCAAGCGCGGAGAGGC 320
 Db 241 CAGTCGGGAACCTGCTGCGCAGTGCATTAATGAATCGGCCAAGCGCGGAGAGGC 300
 QY 321 GGTTCGGTATTTGGCGCTCTTCGGCTTCCTCGCTCACTCACTCGCTGCGCTCGGTCGT 380
 Db 301 GGTTCGGTATTTGGCGCTCTTCGGCTTCCTCGCTCACTCACTCGCTGCGCTCGGTCGT 360
 QY 381 CGGCTCGCGGAGCGGTATCATGCTCACTCAAAAGCGGTAATAGCGTTATCCACAGAAATCA 440
 Db 361 CGGCTCGCGGAGCGGTATCATGCTCACTCAAAAGCGGTAATAGCGTTATCCACAGAAATCA 420
 QY 441 GGGGATAAGCGAGGAAGAACATGTGAGCAAAAGCCAGCAAAAGCGGAGAACCGTAAA 500
 Db 421 GGGGATAAGCGAGGAAGAACATGTGAGCAAAAGCCAGCAAAAGCGGAGAACCGTAAA 480
 QY 501 AAGCGCGGTTGCTGGCGTTTTCATAGGCTCGCGCCCTCGCGCTTATCCAGGATCACAAAAAT 560
 Db 481 AAGCGCGGTTGCTGGCGTTTTCATAGGCTCGCGCCCTCGCGCTTATCCAGGATCACAAAAAT 540
 QY 561 CGACCTCAAGTCAGGTGCGCAACCGCACAGGACTATAAGATACCAAGCGTTTCCC 620
 Db 541 CGACCTCAAGTCAGGTGCGCAACCGCACAGGACTATAAGATACCAAGCGTTTCCC 600
 QY 621 COTGAAGCTCCCTGTCGCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCC 680
 Db 601 COTGAAGCTCCCTGTCGCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCC 660
 QY 681 GCCTTT 686
 Db 661 GNCCTT 666

RESULT 6
 A2540838
 LOCUS ENTET16TF Entamoeba histolytica Sheared DNA linear GSS 14-NOV-2000
 DEFINITION genomic, DNA sequence.
 ACCESSION A2540838
 VERSION A2540838.1 GI:11148010
 KEYWORDS GSS.
 SOURCE Entamoeba histolytica.
 ORGANISM Entamoeba histolytica.
 Eukaryota; Entamoebidae; Entamoeba.
 REFERENCE 1 (bases 1 to 891)
 AUTHORS Loftus B., Van Aken, S. and Fraser, C.
 TITLE Determination of clone end sequences from Entamoeba histolytica
 JOURNAL HMI:IMSS sheared DNA library
 COMMENT Unpublished (2000)
 Contact: Brendan J Loftus
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0208
 Fax: 301 838 3543
 Email: bjoftus@tigr.org
 Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
 DNA library
 Seq primer: M13-Forward
 Class: shotgun

High quality sequence start: 68
 High quality sequence stop: 282.
 Location/Qualifiers
 1. .891

/organism="Entamoeba histolytica"

/strain="HMI:IMSS"

/db_xref="taxon:5759"

/clone_lib="Entamoeba histolytica Sheared DNA"

/note="Vector: pHD1; Site: 1; Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999)."

BASE COUNT 199 a 255 c 213 g 224 t

ORIGIN

Query Match 89.6%; Score 661; DB 12; Length 891;

Best Local Similarity 96.2%; Pred. No. 1.7e-180;

Matches 709; Conservative 0; Mismatches 25; Indels 3; Gaps 3;

QY 5 GACTCACTATAGGCGCAATTCGAGCTCGCTACCGGGGATCCTCTAGAGTCGACCTGCAG 64

Db 1 GACCTACTATTTCGGCAATTCCTAGCTCGGTACCGGGGATCCTCTATAGTCGACCTGCAT 60

QY 65 GCATGCAAGCTTGAGTATTCATAGTGCACCTAAATAGCTTGGCGTAAATCATGTCATA 124

Db 61 GCATGCAAGCTTGAGTATTCATAGTGCACCTAAATAGCTTGGCGTAAATCATGTCATA 120

QY 125 GCTGTTTCTCTGTGAA -ATTGTTATC -GCCTCACAAATTCACACAAATACGAGCCGGA 182

Db 121 GCTGTTTCTCTGTGAAATTTGTTATC TCGCTCACAAATTCACACAAATACGAGCCGGA 180

QY 183 AGCATAAAGTGTAAAGCTGGGTGCTTAATGAGTGAGTAACTCACTCACTAAATTCGCTG 242

Db 181 AGCATAAAGTGTAAAGCTGGGTGCTTAATGAGTGAGTAACTCACTCACTAAATTCGCTG 240

QY 243 CGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTGTCGTCAGCTCATTAATGATCGGC 302

Db 241 CGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTGTCGTCAGCTCATTAATGATCGGC 300

QY 303 CAAGCGCGGGAGAGCGGTTTGGCTATTTGGCGCTCTTCCGCTTCTCGCTCACTGAC 362

Db 301 CAAGCGCGGGAGAGCGGTTTGGCTATTTGGCGCTCTTCCGCTTCTCGCTCACTGAC 360

QY 363 TCGCTGCGCTCGCTGCTGCTGCGGTCGCGGAGCGGTATCAGCTCACTCAAAAGCGGTAATA 422

Db 361 TCGCTGCGCTCGCTGCTGCTGCGGTCGCGGAGCGGTATCAGCTCACTCAAAAGCGGTAATA 420

QY 423 CGGTTATCCACAAATACAGGGGATACGAGGAAAGACATGTGAGCAAAAGCGGCAAGAA 482

Db 421 CGGTTATCCACAAATACAGGGGATACGAGGAAAGACATGTGAGCAAAAGCGGCAAGAA 480

QY 483 AAGCCAGGAACCGTAAAAAGCGCGGTTGCTGGCGTCTTTCATAGCTCCGCCCCCT 542

Db 481 ATGCCAGGAACCGTAAAAAGCGCGGTTGCTGGCGTCTTTCATAGCTCCGCCCCCT 540

QY 543 GAGCAGCATCACAAAAATCGAGCTCAAGTCAAGGTGGCGGCAAAAGCGGCAAGAA 602

Db 541 GAGCAGCATCACAAAAATCGAGCTCAAGTCAAGGTGGCGGCAAAAGCGGCAAGAA 600

QY 603 AGATACAGCGGTTTCCCGCTCGGAAGCTCCCTCGTGGCGCTCTCTGTTCCGACCTCGCG 662

Db 601 AGATACAGCGGTTTCCCGCTCGGAAGCTCCCTCTTGGCGCTCTCTGTTCCGACCTCGCG 660

QY 663 CTTACCGGATACCTGTCGGCTTTCTCCCTTCGGGAAGCTGG-CGCTTTCTCATAGCTC 721
|||||
Db 661 CTTACCGGATACCTGTCGGCTTTCTCCCTTCGGGTACGCTGACGCTTCTCATACTC 720

QY 722 AGCGTGTAGGTATCTCA 738
|||||
Db 721 AGCGGAAGGTTCTCA 737

RESULT 7
LOCUS BE562810 683 bp mRNA linear EST 01-JUL-2001
DEFINITION Arabidopsis thaliana Chronic Ozone Forward-Subtracted Library
ACCESSION BE562810
VERSION BE562810.1 GI:14580073
KEYWORDS EST
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 683)
REFERENCE Eckardt, N.A., Higgins, B.K., Schloss, A. and Fedoroff, N.V.
Subtractive cloning and microarray expression analysis of
ozone-induced genes in Arabidopsis
unpublished (2000)
JOURNAL Contact: Nina V. Fedoroff
COMMENT Biotechnology Institute
Penn State University
519 Wartik Lab, University Park, PA 16802, USA
Tel: 8148635717
Fax: 8148631357
Email: nvf1@psu.edu
Sequence does not include adaptor sequences (corresponding to
Clontech PCR-Select Adaptors 1 and 2R) present on either side of
insert.
Insert Length: 794 Std Error: 200.00
Seq primer: Clontech PCR-Select Nested Primer 2R
High quality sequence start: 26
High quality sequence stop: 708
POLYA-No. Location/Qualifiers
1. 683
/organism="Arabidopsis thaliana"
/cultivar="Columbia"
/db_xref="taxon:3702"
/clone="ATCO2IG4"
/clone_lib="Arabidopsis Chronic Ozone Forward-Subtracted
Library"
/tissue_type="Leaf"
/note="Vector: pT-Adv; PCR Suppression Subtractive
Hybridization library (Clontech PCR-Select). 'Tester' =
RNA pooled from leaf tissue of plants exposed to 3, 6,
and 9 days of ozone at 0.15 uL/L for 6 h/d. 'Driver' =
leaf tissue from control plants maintained in clean air.
Cloned into 3.9 kb AdvantAge vector (Clontech)."
BASE COUNT 157 a 193 c 176 g 155 t
ORIGIN

Query Match 98.6%; Score 653.8; DB 10; Length 683;
Best Local Similarity 98.5%; Pred. No. 1.8e-178;
Matches 669; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 16 GGGCGAATTCGAGCTCGGTACCGGGATCCTCTAGAGTCGACCTGCAGGCATGCAAGCT 75
|||
Db 4 GCGCGAATTCGAGCTCGGTACCGGGATCCTCTAGAGTCGACCTGCAGGCATGCAAGCT 63

QY 76 TGAGTATTTCTATAGTGTACCTCAATAGCTGGCGTAATCATGTCATAGCTGTTTCCTG 135
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Db 64 TGAGTATTTCTATAGTGTACCTCAATAGCTGGCGTAATCATGTCATAGCTGTTTCCTG 123

QY 136 TGTGAATTTGTTATCGGCTCAACAATTCACACAAATTCAGAGCCGGAAGCATAAAGTGT 195
|||||
Db 124 TGTGAATTTGTTATCGGCTCAACAATTCACACAAATTCAGAGCCGGAAGCATAAAGTGT 183

QY 196 AAGCCTGGGTGCTTAATGAGTGAGCTAACTCACAATTAATTTGCTTGGCTCACTGCGCG 255
|||||
Db 184 AAGCCTGGGTGCTTAATGAGTGAGCTAACTCACAATTAATTTGCTTGGCTCACTGCGCG 243

QY 256 CTTTCCAGTCGGGAACCTGTCGTCGCCAGCTGCTTAATGAATGAGCCCAACGCGCGGGA 315
|||||
Db 244 CTTTCCAGTCGGGAACCTGTCGTCGCCAGCTGCTTAATGAATGAGCCCAACGCGCGGGA 303

QY 316 GAGCGGTTTGGGTATTTGGGCGCTCTTTCGGCTTCTCGCTCACTGACTCGGCTGCGT 375
|||||
Db 304 GAGCGGTTTGGGTATTTGGGCGCTCTTTCGGCTTCTCGCTCACTGACTCGGCTGCGT 363

QY 376 TCGTTCGGCTTGGGCGGAGCGGTATCAGCTCACTCAAGGCGGTAAATCGGTTATCCACAG 435
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Db 364 TCGTTCGGCTTGGGCGGAGCGGTATCAGCTCACTCAAGGCGGTAAATCGGTTATCCACAG 423

QY 436 AATCAGGGGATACGCGAAGAAACATGTGAGCAAAAGCCAGCAAAAGCCAGGAACC 495
|||||
Db 424 AATCAGGGGATACGCGAAGAAACATGTGAGCAAAAGCCAGCAAAAGCCAGGAACC 483

QY 496 GTAAAAAGCGCGGTTGCTGCGGCTTTTCCATAGGCTCCGCCCTCGACGAGCATCACA 555
|||||
Db 484 GTAAAAAGCGCGGTTGCTGCGGCTTTTCCATAGGCTCCGCCCTCGACGAGCATCACA 543

QY 556 AATCAGCGCTCAAGTCAGAGGTGGCGAAGCCGACAGACTATAAGATACCGAGCGT 615
|||||
Db 544 AATCAGCGCTCAAGTCAGAGGTGGCGAAGCCGACAGACTATAAGATACCGAGCGT 603

QY 616 TTCCCGCTGGAAGCTCCCTCGGCTCTCTCTGTTCCGAGCCC-TGCCGCTTACCGGATAC 674
|||||
Db 604 TTCCCGCTGGAAGCTCCCTCGGCTCTCTCTGTTCCGAGCCC-TGCCGCTTACCGGATAC 663

QY 675 CTGTCGCGCTTTCTCCCTT 693
|||||
Db 664 CTGTCGCGCTTTCTCCCTT 682

RESULT 8
LOCUS AQ108633 652 bp DNA linear GSS 29-AUG-1998
DEFINITION CIT-HSP-2379M3.TF CIT-HSP Homo sapiens genomic clone 2379M3, DNA
sequence.
ACCESSION AQ108633
VERSION AQ108633.1 GI:3485323
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 652)
ADAMAS, K.D., ROUNSLEY, S.D., ZHAO, S., BASS, S., LINHER, K., GOLDEN, K.,
BERRY, K., GRANGER, D., SUH, E., WIBLE, C., SHIZUYA, H., SIMON, M. and
VENTER, J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
Unpublished (1998)
Other GSSs: CIT-HSP-2379M3.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdamas@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 653)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
Unpublished (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

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DEFINITION BE430218 667 bp mRNA linear EST 24-JUL-2000
CDNA clone SUN000.D12, mRNA sequence.
ACCESSION BE430218
VERSION BE430218.1 GI:9428061
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SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticaceae; Triticum.
1 (bases 1 to 667)
Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier
,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P.,
Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P.,
Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y.,
Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M.,
Sorells,M., Warburton,M. and Wenzel,G.
International Triticaceae EST Cooperative (ITEC): Production of
Expressed Sequence Tags for Species of the Triticaceae
Unpublished (2000)
Contact: Shariflou M
Plant Breeding Institute, University of Sydney
107 Cobbitty Rd., Cobbitty NSW 2570 Australia
Tel: 61 2 9351 8803
Fax: 61 2 9351 8851
Email: mshariflou@pop.usyd.edu.au
International Triticaceae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
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QY 149 TCCGCTCAAAATCCACACATACAGCGCGGAAGCATAAAGTGTAAAGCCTGGGGTGC 208
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Db 181 TTAATGAGTGAAGTAACTACATTAATTTGGTTGGCTCACTGCCGCTTCCAGTCGGG 240
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sequence.
ACCESSION A0057603
VERSION A0057603.1 GI:3354129
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 661)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
Unpublished (1998)
Other_GSSs: CIT-HSP-2345M2.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
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Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45) Fax: 86-21-50801922 Email: hanzg@chgc.sh.cn This clone is available at CHGC in Shanghai.									
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QY	340	CTTCCGCTTCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGT	399						
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hematopoietic necrosis virus Oncorhynchus mykiss cdna clone KA9,
mRNA sequence.
ACCESSION
VERSION AU081040
KEYWORDS
SOURCE rainbow trout.
ORGANISM
Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE
1 (bases 1 to 1039)
AUTHORS Kono,T., Sakai,M. and LaPatra,S.E.
TITLE Expressed Sequence Tag Analysis of Kidney and Gill Tissues from
Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious
Hematopoietic Necrosis Virus
JOURNAL Mar. Biotechnol. 2 (5), 493-498 (2001)
COMMENT Contact: Masahiro Sakai
Faculty of Agriculture
Miyazaki University
1-1 nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan
Email: m.sakai@cc.miyazaki-u.ac.jp.
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hematopoietic necrosis virus Oncorhynchus mykiss cdna clone KG'12,
mRNA sequence.
ACCESSION
VERSION AU081124
KEYWORDS
SOURCE rainbow trout.
ORGANISM
Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE
1 (bases 1 to 1089)
AUTHORS Kono,T., Sakai,M. and LaPatra,S.E.
TITLE Expressed Sequence Tag Analysis of Kidney and Gill Tissues from
Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious
Hematopoietic Necrosis Virus
JOURNAL Mar. Biotechnol. 2 (5), 493-498 (2001)
COMMENT Contact: Masahiro Sakai
Faculty of Agriculture
Miyazaki University
1-1 nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan
Email: m.sakai@cc.miyazaki-u.ac.jp.
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Db 681 GTGGCGCTTTCATAGCTCAGCTGTAGGTATCTCA 717

RESULT 15
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DEFINITION
AU081044 Oncorhynchus mykiss 1163 bp mRNA linear EST 30-AUG-2001
hematopoietic necrosis virus Oncorhynchus mykiss CDNA clone K81,
mRNA sequence.
ACCESSION
VERSION AU081044.1 GI:6431392
KEYWORDS EST.
SOURCE rainbow trout.
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE
Kono, T., Sakai, M. and LaPatra, S.E.
Expressed Sequence Tag Analysis of Kidney and Gill Tissues from
Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious
Hematopoietic Necrosis Virus
Mar. Biotechnol. 2 (5), 493-498 (2001)
CONTACT: Masahiro Sakai
Miyazaki University
1-1 nishi gakukenbanaadai, Miyazaki, Miyazaki 889-2192, Japan
Email: m.sakai@cc.miyazaki-u.ac.jp.
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QY 642 TCTCTGTTCGGACCTTCGGCTTACGGATACCTTCGGCTTTCCTCCCTTCGGGAAAGC 701
Db 905 TCTCTGTTCGGACCTTCGGCTTACGGATACCTTCGGCTTTCCTCCCTTCGGGAAAGC 964
QY 702 GTGGCGCTTTCATAGCTCAGCTGTAGGTATCTCA 738
Db 965 GTGGCGCTTTCATAGCTCAGCTGTAGGTATCTCA 1001

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Search completed: August 1, 2002, 08:39:59
Job time: 6490 sec

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Thu Aug 1 12:08:51 2002